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Copyright (c) 1993 - 2000 Compugen Ltd.
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			Description	A surface protein	BASB029 amino acid	N. meningitidis EG	A surface protein	N. meningitidis BZ	A surface protein	N. meningitidis H1	A surface protein	N. meningitidis BZ	BASB029 amino acid	A surface protein
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SUMMARIES			ID	AAY23740	AAY57044	AAU06174	AAY23739	AAU06179	AAY23742	AAU06177	AAY23738	AAU06178	AAY57045	AAY23743
			DB	20	21	22	20	22	20	22	20	22	21	20
			Match Length DB	594	594	594	594	594	598	598	598	598	591	599
	dР	Query	Match	100.0	100.0	100.0	95.2	95.2	94.6	94.6	94.5	94.5	92.2	91.5
			Score	3019	3019	3019	2874	2874	2855	2855	2852	2852	2783.5	2762.5
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r.	91.4	91.4	91.4	91.1	90.7	20.1	87.3	87.3	83.9	83.4	83.4	82.9	81.1	79.8	78.4	73.9	67.3	62.5	44.0	42.8	34.9	34.8	34.1	32.4	32.4	24.5	24.1	22.8	22.8	19.7	13.1	13.0
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# ALIGNMENTS

G.	ID AAY23740 standard; Protein; 594 AA.
AC X	AAY23740;
X E	08-SEP-1999 (first entry)
X E	A surface protein of Neisseria meningitidis.
K K K	Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.
SOS	Neisseria meningitidis.
XZ	W09931132-A1.
X C :	24-JUN-1999.
PF	14-DEC-1998; 98WO-AU01031.
X K	12-DEC-1997; 97GB-0026398.
A P P P	(ISIS-) ISIS INNOVATION LTD. (UYQU ) UNIV QUEENSLAND.
VV Id	Jennings MP, Moxon ER, Peak IRA;
N N N	WPI; 1999-418754/35. N-PSDB; AAX85792.
PT	Neisseria meningitidis sürface proteins useful for treating meningitidis infections
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/note= "Encoded by AATC"

99WO-EP03255

07-MAY-1999;

WO9958683-A2

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Neisseria meningitidis

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                         The present sequence represents a surface protein of Neiserria menigitidis which is approximately 62 KDs. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis auffection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                              LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
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Claim 1; Page 100-101; 132pp; English.
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Matches 594; Conserv
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This is the Nisseria meningitidis BASB029 amino acid sequence from scroproup B strain ATCC13090. The BASB029 protein is homologous to the lamemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and polypeptide sequences (AAZ39864-Z39865) and polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the strengely for the stimmune system of an organism creased recombinant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH 180
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100.0%; Pred. No. 5.1e-173;
Live 0; Mismatches 0;
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                                                    TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK
                                                                            PVRITHNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPG
                                                                                                                                                                              N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                          Surface antigen NhhA; meningococcal disease; meningitis vaccine.
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Mismatches 0;
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Peak IRA, Jennings
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Matches 594;
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421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK 480
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                                301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA 360
                                               361 TVSKDDOGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE 420
                                                                                          N. meningitidis B2198 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                       Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                                                 /label= C5
/note= "Conserved region 5"
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/note= "Conserved region 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                      AAU06179 standard; Protein; 594 AA
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/label= V1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PVORTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally surface glycoproteins, nucleic acids, the primers and optionally the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.2%; Score 2874; DB 20; Length 594; Best Local Similarity 95.6%; Pred. No. 2.5e-164; Matches 568; Conservative 5; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis surface proteins useful for treating N. meningitidis infections
                   541 ksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgygw 594
                                                                                                                                                                 Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.
                                                                                                                                               A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 95-97; 132pp; English.
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                                                                                AAY23739 standard; Protein; 594
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                                                                                                                                                                                                            Neisseria meningitidis.
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N-PSDB; AAX85791.
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Pred. No. 2.5e-164;
5; Mismatches 21;
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95.6%;
25-JAN-2000; 2000US-0177917
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Best Local Similarity 95.6
Matches 568; Conservative
                            (UYQU ) UNIV QUEENSLAND.
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                                                                                                                                                                                                                                                                                                                                                                            Surface protein; surface glycoprotein; infection; vaccine;
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Pred. No. 3.4e-163;
6; Mismatches 22;
                                                                                                                                                                                                                                                                                                                           surface protein of Neisseria meningitidis
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ilarity 94.6%;
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                                                                                                                                                                                                                                                                                                                                                                Surface antigen NhhA; meningococcal disease; meningitis vaccine
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/note= "Conserved region 4"
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/note= "Conserved region 5"
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/note= "Conserved region 1"
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophlactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the Wild type surface antigen Nhh from N. meningitidis strain H15 is 1 of 10 NhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
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                                                                                                                                                                                                                                                                                                     New Nhhk surface antigen polypeptides and polynucleotides from Messeria meingitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120
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94.6%; Score 2855; DB 22; Length 598;
Best Local Similarity 94.6%; Pred. No. 3.4e-163;
Matches 566; Conservative 6; Mismatches 22; Indels 4
Matches 566; Conservative 7.
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25-JAN-2000; 2000US-0177917.
                                                                      (UYQU ) UNIV QUEENSLAND.
                                                                                                                                    Peak IRA, Jennings MP;
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481 dankpvritnvapgvkegdvtnvaqlkgvaqnlnnridnvdgnaragiaqaiataglaqa 540
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              The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerse, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to least to identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                         treating
                                                                                                                                           glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                        useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2852; DB 20;
Pred. No. 5.2e-163;
5; Mismatches 23;
                                                                                                                          A surface protein of Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                          surface proteins
                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 91-93; 132pp; English.
                                                                         AAY23738 standard; Protein; 598 AA.
                                                                                                                                                                                                                                                                               Peak IRA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.5%;
                                                                                                                                                                                                                    98WO-AU01031.
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                                                                                                                                                                                                                                     97GB-0026398
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 94.6
56; Conservative
                                                                                                                                           Surface protein; surface
                                                                                                                                                                                                                                                                               Moxon ER,
                                                                                                                                                                                                                                                              QUEENSLAND
                                                                                                                                                                                                                                                                                                                                 meningitidis infections
                                                                                                                                                   immunoreactive peptide.
                                                                                                                                                                   Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                         meningitidis
                                                                                                                                                                                                                                                                                              WPI; 1999-418754/35.
N-PSDB; AAX85790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   598 AA;
                                                                                                                                                                                                                                                     SISI (-SISI)
                                                                                                                                                                                   WO9931132-A1.
                                                                                                                                                                                                                                                                               Jennings MP,
                                                                                                                                                                                                                    14-DEC-1998;
                                                                                                                                                                                                                                     12-DEC-1997;
                                                                                                          08-SEP-1999
                                                                                                                                                                                                    24-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266;
                                                                                                                                                                                                                                                                                                                         Neisseria
                                                                                         AAY23738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
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                                                                AAY23738
                                                         RESULT
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GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 356
                                                                                                   GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 416
                                                                                                                                                    KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK 476
                                                                                                                                                                                                                                        DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQA 536
                                                                                                                                                                                                                                                                                       NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N. meningitidis BZ10 surface antigen NhhA polypeptide sequence.
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/label- Cl
/note- "Conserved region 1"
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|131..194
|/label= C3
|---= "Conserved region 3"
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/norte= "Conserved region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label = C2
note= "Conserved region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tabel= V2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195..216
/label- V3
/note= "Variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label='V4
/note= "Variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             AAU06178 standard; Protein; 598 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis strain BZ10
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Surface antigen
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477 DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQA 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA MANDIGIBO. The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in alianostics, therapeutic and problactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain E2010 is 1 of 10 NhA Polypeptide sequences (AAUG6171-AAUG6180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NTNA----SSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Fig 1; 91pp; English.
                                                        25-JAN-2001; 2001WO-AU00069.
                                                                                                                25-JAN-2000; 2000US-0177917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.6
Matches 566; Conservative
                                                                                                                                                                         (UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                                 Peak IRA, Jennings MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention.
                                                                                                                                                                                                                                                                                   WPI; 2001-488774/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 598 AA;
                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS09168
02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
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This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain H4476. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polyynoloclocitée sequences (AAZ39864-239865) and polypeptides sequences (AAZ39864-x27865) and theair immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polymuclectide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the
                                                                                                                                                                                                                                                                      BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.
537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                             New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
                                                                                                                                                                                                                                          BASB029 amino acid sequence from N. meningitidis strain H44/76.
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Encoded by AAC"
Misc-difference 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Encoded by AATC"
                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Encoded by GAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Encoded by ACA"
                                                                                                                                                                                                                                                                                                                                                                               /note= "Encoded by AAT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Encoded by CGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                   AAY57045 standard; Protein; 591 AA.
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                                                                                                                                                                                                           21-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis.
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Misc-difference 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
Misc-difference 269
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Misc-difference 389
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N-PSDB; AAZ39865.
                                                                                                                                                                                                                                                                                                                                                              Misc-difference 90
                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 92
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                                                                                                                                                                               AAY57045;
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AAY57045
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polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism
                                                                                                                                                                                                                                                                                                                                                                    DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQA 536
                                                                                                                                                                                                                                                                                                                                                                                                               YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ 116
                                                                                                                                                                                                NTNENTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGD 176
                                                                                                                                                                                                        TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236
                                                                                                                                                                                                                                          SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDK 296
                                                                                                                                                                                                                                                                           GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 356
                                                                                                                                                                                                                                                                                                            GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 416
                                                                                                             Gaps
                                                                                                                                       MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD---DDDL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                       YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 591;
                                                                                                             11;
                                                                                            Score 2783.5; DB 21; Lengt
Pred. No. 6.5e-159;
9; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycoprotein; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A surface protein of Neisseria meningitidis
                                                                                             52.2%;
al Similarity 93.3%;
558; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY23743 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis
                                                   the protein.
                                                                    591 AA;
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                                                   receiving
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                                                                     Sequence
                                                                                             Query Match
Best Local 9
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                                                                                                             Matches
                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     536 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD-DDDLYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                          Neisseria meningitidis surface proteins useful for treating meningitidis infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.5%; Score 2762.5; DB 20
91.7%; Pred. No. 1.2e-157;
ive 13; Mismatches 32;
                                                                                                                                                                                                                                                                                                         Claim 1; Page 114-115; 132pp; English.
                                                                                                                                             Peak IRA;
                                                                                  LTD.
                                          97GB-0026398
    98WO-AU01031
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Matches 549; Conservative
                                                                                INNOVATION
                                                                                                   QUEENSLAND
                                                                                                                                           Moxon ER,
                                                                                                                                                                                 WPI; 1999-418754/35.
N-PSDB; AAX85795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       599 AA;
                                                                                                                                           Jennings MP,
                                                                              VINU (UYU)
14-DEC-1998;
                                        12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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599 AA;

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diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain H38 is 1 of 10 NhhA polypeptide sequences (AAU06180) from 10 different N. meningitidis strains given in
                                                                                         the present invention.
                                                                                                                Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhAA (AAU06182-AAU06186). The modified or mutant NhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Nhha surface antigen polypeptides and polynucleotides from besseria meningitudis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
 Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                   N. meningitidis H38 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                      "Conserved region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Conserved region 4"
                                                                                                                                                                                                                                     "Conserved region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Variable region 4"
                                                                                                                                                                                                                                                                                                                                       "Variable region 2"
                                                                                                                                                                                                                                                                     'note= "Variable region 1"
                                                                                                                                                                                                                                                                                                                                                                                                        "Variable region 3"
                                                                                                                                                                                                    Location/Qualifiers
                                                                 AAU06176 standard; Protein; 599 AA
                                                                                                                                                                              Neisseria meningitidis strain H38.
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                                                                                                             24-OCT-2001
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61 epvvrsalvlqfmidkegngenestgnigwsiyydnhntlhgatvtlkagdnlkikqntn 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 KGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG 355
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                                              Gaps
                                                                                                        1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD-DDDLYL 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis; bacterial infection; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 91.7%; Pred. No. 1.2e-15;
Best Local Similarity 91.7%; Pred. No. 1.2e-15;
Matches 549; Conservative 13; Mismatches 32; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of N. meningitidis protein ORF40-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
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                                                                                                                                                                                                                                                                               The invention provides proteins (AAY27201-245) from Neisseria meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition or a diagnostic composition. The composition is also useful for treating or preventing an infection due to Neisserial bacteria, especially Neisseria meningitidis.
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                                                                                                                                                                                                                    diagnostic compositions for treating and/or preventing Neisseria meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20; Length 591;
                                                                                                                                                                                                          useful in vaccines
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                                                                                                                                               Scarlato
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; Pred. No. 2e-157
14; Mismatches
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                                                                                                                                                                                                          New protein and its nucleotide sequence,
                                                                                                                                               Pizza M,
                                                                                                                                                                                                                                                         Claim 1; Page 62; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      91.4%;
                                                                     98GB-0022143.
98GB-0000760.
98GB-0019015.
                                               99WO-IB00103
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.4
Best Local Similarity 92.3
Matches 552; Conservative
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                                                                                                                                             Masignani
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N-PSDB; AAX99124.
                                                                                                                      (CHIR-) CHIRON SPA.
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W09936544-A2
                                              14-JAN-1999;
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                        537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence represents a surface protein of Neiserria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis surface proteins useful for treating
                                                                                                                                                                                                                                                                                                                                                 surface glycoprotein; infection; vaccine;
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21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.4%; Score 2758.5; Di
92.3%; Pred. No. 2e-157,
ive 14; Mismatches
                                                                                                                                                                                                                                                                                                 A surface protein of Neisseria meningitidis.
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                                                                                                                                                          AAY23746 standard; Protein; 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moxon ER,
                                                                                                                                                                                                                                                                                                                                                                       immunoreactive peptide
                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                    175 ttvhlngigstltdtllntgattnvtndnvtddekkraasvkdvlnagwnikgvkpgtta 234
                                     SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDK 296
                                                                                                                                                                                         GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                           N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Surface antigen NhhA; meningococcal disease; meningitis vaccine.
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/label= Mature_NhA
/label= mredicted mature protein, specifically
/note= "Predicted in claim 12"
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/note= "Conserved region 1"
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/note= "Conserved region 4"
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/note= "Variable region 4"
237..591
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/label= C.
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA MANO6182-AAV06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain PMC21 is 1 of 10 NhhA polypeptide sequences (AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 YLEPVORTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/label= C5
/note= "Conserved region 5"
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                                                                                                                                                                                                                 25-JAN-2001; 2001WO-AU00069
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N-PSDB; AAS09161.
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Best Local Similarity
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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
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GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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115-09-377-155-9			Query Match 100.0%; Score 3019; DB 4; Length 594;	Similarity 100.0%; Pred. No. 1.5e-226;	vative 0;		Qy 1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60		Db 1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60		Oy 61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVÝFDKKGVLTAGTITLKAGDNLKIKQNTNE 120		Db 61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120		Qy 121 NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH 180		Db 121 NTNASSETYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH 180		Qy 181 LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240		Db 181 LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240		Qy 241 DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGEND 300		Db 241 DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGEND 300		QY 301 SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA 360	
******************	Sequence 9, Appli	ence 9,	ence 7,	ence 7,	ence	Sequence 13, Appl	ence	ence	ence	ence.15,	ence 21,	ence 21,	ence 2, 1	ence 2,	Sequence 11, Appl	ence	ence 17,	ence 17,	ence	ence 19,	ence 33,	ence 4, 7	ence	ence	ence	ence	Sequence 6, Appli	
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michard
TITLE OF INVENTION: UNVEL SURRACE ANTIGEN
FILE REPERBNCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: US/09/77,155
PRIOR FILING DATE: 1999-08119
PRIOR FILING DATE: 1999-08119
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER: OF SEQ ID NOS: 33
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                             RESULT 2
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6333173
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JS-09-669-974-9
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Les 594; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PERK, Ian Richard Anselm APPLICANT: PERK, Ian Richard Paul APPLICANT: PERNINGS, Michael Paul TITLE OF INVENTION: NOVEL, SURFACE ANTIGEN TITLE OF INVENTION: NOVEL, SURFACE ANTIGEN CURRENT FILE OF 1999-08-19 CURRENT FILING DATE: 1999-08-19 PRIOR FILING DATE: 1997-12-12 PRIOR FILING DATE: 1997-12-12 NUMBER: CSEQ ID NOS: 33

SEQ ID NO 7
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US-09-377-155-7
Sequence 7, Application US/09377155
; Patent No. 6197312
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; ORGANISM: Neisseria meningitidis
US-09-377-155-7
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361 TVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE 420
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Pred. No. 8.5e-214;
6; Mismatches 22;
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94.6%;
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Best Local Similarity 94.6
Matches 566; Conservative
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        PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE
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Pred. No. 2.8e-215;
5; Mismatches 21;
                                                                                                                                                                                                                                        Sequence 7. Application US/09669974

Fatent No. 6333173

GENERAL INFORMATION:
APPLICANT: PERK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PARCHIN VET. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Neisseria meningitidis
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95.6%;
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Best Local Similarity 95.6
Matches 568; Conservative
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US-09-669-974-7
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US-09-669-974-7
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477 DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQA 536
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                                                                                                                               537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
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94.6%; Score 2855; DB 4; Length 598;
Best Local Similarity 94.6%; Pred. No. 8.58-214;
Matches 566; Conservative 6; Mismatches 22; Indels
                                                                                                                                                                                                                                                                   APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENKINGS, Michael Paul
APPLICANT: DENKINGS, Michael Paul
APPLICANT: WOXON, E. Richard
TITLE OF INVENTION: ROYEL SURFACE ANTIGEN
FILE REFERENCE: 06504/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: US/09/71/155
PRIOR PELLING DATE: 1999-09-19
PRIOR FILING DATE: 1999-10-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
SRIOR APPLICATION NUMBER: PGT/AU98/01031
PRIOR FILING DATE: 1999-12-14
SRIOR APPLICATION NUMBER: PGT/AU98/01031
SOSTWARE: PALGENTING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOSTWARE: PALGENTIN VET: 2.0
                                                                                                                                                                                                                          Sequence 13, Application US/09669974 Patent No. 6333173
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US-09-669-974-13
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Best Local Similarity
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                                                                                                                                                                                            RESULT 6
US-09-669-974-13
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                                                                                                                                                                                    61 PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
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                                                                                                                                                                                                                                                                                                                                        537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                                                                                                                                                                                                                                                                                                                                                                           94.5%; Score 2852; DB 4; Length 598; ilarity 94.6%; Pred. No. 1.5e-213; Conservative 5; Mismatches 23; Indels 4
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APPLICANT: PEAK, Ian Richard Paul
APPLICANT: PEAK, Ian
APPLICANT: PENNINGS: Michard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REPERENCE: 065.064/0128
CURRENT FILING DATE: 1999-081-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1999-081-19
PRIOR FILING DATE: 1997-12-12
NUMBER: OF SEQ ID NOS: 33
SEQ ID NO S
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; ORGANISM: Neisseria meningitidis
US-09-377-155-5
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Pred. No. 1.3e-206;
                                                                                                                                                            APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. R. RICHARD CURRENT APPLICATION NUMBER: US/09/377,155 CURRENT APPLICATION NUMBER: PCT/AUG8/01031 PRIOR APPLICATION NUMBER: GB 9726398.2 PRIOR FILING DATE: 1999-101.12 PRIOR FILING DATE: 1997-112-12 NUMBER OF SEO ID NOS: 33 SOFTWARE: Patentin Ver: 2.0
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                                                                                                          US-09-377-155-15; Sequence 15, Application US/09377155; Patent No. 6197312
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; ORGANISM: Neisseria meningitidis
US-09-377-155-15
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Best Local Similarity
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Pred. No. 1.5e-213;
5; Mismatches 23;
                                                                                                                                                            APPLICANT: PEAK, Ian Richard Anselm APPLICANT: PEAK, Ian Richard Anselm APPLICANT: DEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul III. SEPERENCE: O65064/0128 US/09/669,974 CURRENT APPLICATION NUMBER: US/09/669,974 CURRENT FILING DATE: 1999-08-19 PRIOR APPLICATION NUMBER: US/09/77,155 PRIOR PILING DATE: 1998-12-14 PRIOR PILING DATE: 1998-12-14 PRIOR PILING DATE: 1998-12-14 PRIOR PILING DATE: 1999-12-12 NUMBER: GB 9726398.2 NUMBER: OF SEQ ID NOS: 33 SEQ ID NOS: 33 SEQ ID NOS: SEQ ID NOS: 20
                                                                                                                                    Sequence 5, Application US/09669974
Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-5
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Best Local Similarity 94.6%;
Matches 566; Conservative 5
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US-09-669-974-5
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91.5%; Score 2762.5; DB 4; Length 599;
Best Local Similarity 91.7%; Pred. No. 1.3e-206;
Matches 549; Conservative 13; Mismatches 32; Indels 5;
                                                                                              GENERAL INFORMATION:
APPLICANT: PERK, I an Richard Anselm
APPLICANT: PERK, I an Richard Anselm
APPLICANT: DEMNINGS, Michael Paul
APPLICANT: MOXON E. Richard
ITILE OF INVENTION: NOVEE SURFACE ANTIGEN
FILE REPRENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT PLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: CO09-26
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
SPRIOR FILING DATE: 1991-12-12
NUMBER OF SEQ ID NOSE: 33
SOSTWARE: PATENTIN VOR: 2.0
                                                                        Sequence 15, Application US/09669974 Patent No. 6333173
                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15
                                               RESULT 10
US-09-669-974-15
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58 YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ 116
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                                                                                                                                                                                         APPLICANT: PERK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 055064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR PELLICATION NUMBER: PCT/AU98/01031
PRIOR PELLICATION NUMBER: GB 9726398.2
PRIOR PELLICATION NUMBER: GB 9726398.2
                                                                        RESULT 11
US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
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US-09-377-155-21
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SOFTWARE: PatentIn Ve
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LENGTH: 591
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92.3%; Pred. No. 2.6e-206;
iive 14; Mismatches 21;
                                                      APPLICANT: PEAK, Ian Richard Anselm APPLICANT: DENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, EN Richard CHURCANT: MOXON, EN RICHARD CURRENT APPLICATION NUMBER: US/09/669,974 CURRENT PILING DATE: 1999-08-19 PRIOR APPLICATION NUMBER: PCT/AU98/01031 PRIOR FILING DATE: 1999-08-19 PRIOR FILING DATE: 1999-08-19 PRIOR FILING DATE: 1997-12-12 NUMBER OF SEQ ID NOS: 33

SOFTWARE: PARCHING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 33

LENGTH: 591
               Sequence 21, Application US/09669974 Patent No. 6333173
                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Neisseria meningitidis
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Best Local Similarity 92.39
Matches 552; Conservative
                                               GENERAL INFORMATION:
US-09-669-974-21
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                                                  APPLICANT: DEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MONON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER: OF SEQ. ID NOS: 33
NUMBER: OF SEQ. ID NOS: 33
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2, Application US/09377155
5. 6197312
                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis
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92.0%;
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                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     NUMBER SOFTWARE: Pate SEQ ID NO 2
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US-09-669-974-2
                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: N6
US-09-377-155-2
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Best Local 9
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57 LYLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTLTLKAGDNLKIK 115
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 GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON. E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
SOFTWARE: PALENTIN NUMBER: GB 9726398.2
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALENTIN VOY: 2.0
SEQ ID NO 2
LENGTH: 592
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Patent No. 6197312
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        ORGANISM: Neisseria meningitidis US-09-669-974-2
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Best Local Similarity 92.09
Matches 551; Conservative
GENERAL INFORMATION:
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US-09-377-155-11
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58 YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 -----NGTNETYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQA 536
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                                                                                                                                                                                                                                                                                                                                                                                                                              537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.7%; Score 2739.5; DB 4; Length 591;
ilarity 91.8%; Pred. No. 7.96-205;
Conservative 15; Mismatches 23; Indels 11;
APPLICANT: PEAK, Ian Richard Anselm APPLICANT: BINNINGS, Michael Paul SPEDIICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN TITLE OF INVENTION: NOVEL SURFACE ANTIGEN CURRENT APPLICATION NUMBER: US/09/377,155 CURRENT FILING DATE: 1999-08-19 PRIOR APPLICATION NUMBER: PCT/AU98/01031 PRIOR FILING DATE: 1998-12-14 PRIOR FILING DATE: 1997-12-12 NUMBER OF SEQ ID NOS: 33 SOCTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-11
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 549; Conserv
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Search completed: September 5, 2002, 10:23:46
Job time: 283 sec

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Thu Sep

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 5, 2002, 10:20:33 ; Search time 34.15 Seconds
(without alignments)
1671.364 Million cell updates/sec

US-09-700-293-2 3019 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASSVGYQW 594 Title: Perfect score: Sequence:

Scoring table:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	adhesin NMB0992 [i	probable surface f	adhesin homolog HI	surface protein XF	surface protein XF	probable autotrans		probable adhesin E	probable surface p	cal prot	surface-exposed on	190K surface antig	probable adhesin P	high-molecular-wei	adhesin AIDA-I pre	īd		hypothetical prote	AidA-I adhesin-lik	probable adhesin Z	probable autotrans	high-molecular-wei	probable adhesin h	probable RTX famil	hypothetical prote	AidA-I adhesin-lik	probable beta-barr	sapB protein - Cam	hemolysin A precur
SUMMARIES	. OI	,		164138				-				-		H83135		S28634	T31105	A64905	AG2560	D90803	H85611	AD0123	B43855	AF0394	B85547	F90696	B90674	$^{\circ}$	0	A35140
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æ	Query	91.4	83.9	20.5		12.7	12.4	12.2		11.0	8.1	•	7.4	7.4	7.3	7.3	7.3	7.2	7.2	7.1	7.1	7.1	٠		•	6.9	6.9		9.8	9.9
	Score	2758.5	2533	620	398.5	384.5	375.5	",	368.5	33		239	224	222	220	219	219	216.5	$\sim$	214.5	214.5	213	211.5	209.5	209	209	208	208	205.5	204.5
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hypothetical prote	hemolysin A - Serr	hypothetical prote	surface-array prot	hypothetical prote	probable flagellin	probable structura	probable invasin Y	ABC-type transport	hypothetical prote	hypothetical prote	outer membrane pro	hypothetical prote	filamentous hemagg	surface array prot	hypothetical prote
D85724	A28182	AH2515	A56143	E90893	н90681	D85532	AB0480	C48399	B98047	S76109	T30852	A83080	T31102	140614	A83412
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6.7	6.7	6.7	6.7	9.9	9.9	9.9	9.9	9.9	6.5	6.5	6.5	6.5	6.4	6.4	6.4
203.5	203	203	201.5	200.5	200	200	200	198	197	197	195	195	194.5	194	194
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

	Qy       473 VGSKDANKPVRITHVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAG 532         Db       471 VGSKDANKPVRITHVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 530         Qy       533 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY 592         Qy       531 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY 590         Qy       593 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY 590         Qy       593 QW         Sy       60         Qy       591 QW         Sy       60         FESULT       3
RESULT 2 A81888 Probable surface fibril protein NWA1200 [imported] - Neisseria meningitidis (strain 2249 c'Species: Neisseria) C'Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C'Species: Neisseria May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C'Species: Neisseria May-2000 #sequence of strain 05-May-2000 #text_change 02-Feb-2001 Nature 404, 502-506, 2000 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491. A;Accession: A81888 A;Status; preliminary A;Molecule type: DNA A;Residues: 1-592 c-PAR> A;Molecule type: DNA A;Residues: 1-592 c-PAR> A;Eversimental source: serogroup A; strain 22491 A;Experimental source: serogroup A; strain 22491	n homolog HII732 - Haemophilus in les: Haemophilus influenzae : 18-Aug-1955 #sequence_revision saion: 164138 white schmann, R.D.; Adams, M.D.; White yne, J.D.; Scott, J.; Shirley, R.; Brandon, R.C.; Fine, L.D.; Fritte 269, 496-512, 1995 ors: Gnehm, C.L.; McDonald, L.A.; e: Whole-genome random sequencing rence number: Add000; MUID:953506 us: nucleic acid sequence not shoule type: DNA dues: 1298 <tigr></tigr>
C;Genetics: A;Gene: NWA1200	Query Match 20.5%; Score 620; DB 2; Length 298; Best Local Similarity 46.6%; Pred. No. 2e-24; Matches 145; Conservative 41; Mismatches 91; Indels 34; Ga
Query Match B83.9%; Score 2553; DB 2; Length 592; B885 Local Similarity 86.4%; Pacch No. 3.2e-120; Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6; Qy I MNXIXRIIWNSALNAWVAVEBLTRNHTKRASATVATAVLEFATVQASTTD-DDDLYL 59	OY 1 MMKTRYINNSALNAWVANSELTRHAFKRASATVARALATULATURATADDDLYLE 60 1
	100 - DQGGKSVTFFALKDLYBLDSWAYFEDNAULTRATTSBEARGESTATKAULTRATTSBEARGESTATKAULTRATTSBEARGESTATKAULTRATTSBEARGESTATKAULTRATTSBEARGESTATKAULTRATTSBEARGESTATKAULTBEARGESTATKAUL
OY 115 KONTNENTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETN 174	173
173 GDTTVHLNGIGSTLIDILLINIGATINVTNDNYTDDEKRADSVRDLINGANIKVRYGGT 173 GDTTVHLNGIGSTLIDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGS 235 TASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVT 	GTJASDNOÞFYRTVDTVEELSADTKTTYNVBEKNOKKTEKKIGAKTSVLYKTEKDKLYT ::
OY 293 GKDKGENDSSTDKGEGLVTAKEVIDAVNKAGWRWKTTTANGCTGQADKFETVTSGTNVTF 352	PESULT 4  D82671  surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)  C; Species: Xylella fastidiosa C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C; Accession: D82671 R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000 A; Title: The garones sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A82315; MUID:20365717 A; Note: for a complete list of authors see reference number A59328 below

14:35:59

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Thu Sep

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A; Cross-references: GB:AB003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001
A; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
B; Simpson, A.J.G.; Relaach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, B as-Neto, E.; Docena, C.; El-Dorry, H.; Fraga, J.S.; Franca, S.C.; Franco, D.M.; Carrer, E as-Neto, E.; Docena, C.; El-Dorry, H.; Fraga, J.P.; Krieger, J.E.; Kriener, E.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Remper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, A.M.B.N.; Matsukuma, A.Y.; Menck, C.E.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.E.; Marques, M.V.; Martins, E.M.; de N.; de Allada, M.C.; de Oliveira, M.C.; de Oliveira, R.C.; Santelli, R.V.; Salvas, A.G.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, R.A.; Contents: annotation
C; Genetics: Algene: XF1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1397 VTAGTEETDAVNFSQLKSISTAVDQGWTLTASGANGSKVAS----GGTVDLKN--TDGNL 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGVG------TQASGEGAAA-----VGSG---AAASGKGSTAIGRNAIASADGSVAL 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1945 VTNVAAGTADTDAVNVSQLNQGLITAKQYTDGMVGNLRRETSGGVAAAIATANLPQAYVQ 2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TL-KAGDNLKIKQNTNENTNASSFTY---SLKKDLTDLTS---VGTEKLSFSANSNKVNI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 VQASTIDDDDLYLEPVQ--RTAVVLSFRSDKEGIGEKEVIEDSNWGVYFDKKGVLTAGII 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 TYDTVEFLSADTK-----TTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 IDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 219;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 13.2%; Score 398.5; Best Local Similarity 24.5%; Pred. No. 3.2e Matches 175; Conservative 100; Mismatches
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2059 <SIM>
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C; Jacces 18 Ang-Zulou Fsequence_revision 20-Aug-Zulou Ftext_Change 20-Aug-Zulou C; Jaccession: A82615
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 153-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717
A; Reference number: A82515; MUID:20365717
A; Recension: A82616
A; Status: preliminary
A; Recension: A82616
A; Status: preliminary
A; Recension: A82616
A; Status: preliminary
A; Residues: 1-1190 <SIM>A; Residues: 1-1190 <SIMA <A; Residues: 1-1190 <A; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Simpson, A.J. G.; Reinach, F.C.; Arruda, A.J. S.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A; Carraro, D.M.; Sunques, J.C.B.; Vandeira, A.J. S.
Submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, J.S.; Kuramae, E.E.; La chado, M.A.; Madeira, M.M.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Madeira, M.A.; Madeira, M.A.; Madeira, M.A.; Madeira, M.A.; Madeira, M.A.; Sulva, A.M.; Silva, J.M.; Silva, A.M.; A.C.; Silva, A.M.; Silva, A.M.; Silva, A.M.; Silva, A.M.; Silva, A.M.; A.C.; Silva, A.M.; A.C.; Silva, A.M.; Silva, A.C.; Silva, A.M.; Silva, A.M.; Silva,
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                                                                                                                                                                                                                                                            surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     742 DLKNTDGNIVISKESGSNDVLFNLSSSLKLDKLTVGDTVMTTNGV-----TVGSGVTL 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  630 TIDSNDVTFN-----LATALKVDSLTTGNTAMTTDGVTVGSN--VTLGSTGLVITDGPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    682 VISSGISAGNOKITNVAAGTADTDAVNFSQLOAVSSTASKGWNLLASGANSSNVAPGESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851 YYSTYD-----GGTQGGNYNGDGATGTRSIAVGVGTLASAEGATAVGSGAAASGKGSTA
2005 GRGMTSVGVSSYQGQSAIAVGVSAVSESGHWVFKFSGSANTRSHVGVGAGVGYQW 2059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 FVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTS---VIKEKDGKLVTGKDK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 25.2%
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: XF1981
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950 VGDASKGETRTVS----NVADAKEAT--DAVNLRQLDRVAQDANRYVDNKIESLSEGQT 1002

ISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADA----

407

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297 -GEN-----DSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNV 350

905 IGRNAVASADGSVALGDGA------KDGAR----GAESYTGKYSGLQNNTVGTVS

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351 TFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQL----QNSGWNLDSKAVAGSSGKV

OY 369NITUMYDVNVGDALNVN	RESULT 7 886036 Probable a C. Species: 16 C. Accession Allier, L. Andrews A. Reference A. Reference A. Reference A. Status: A. Residues A.	Ouery Match Best Local Similarity 23.0%; Pred. No. 7.4e-11; Matches 174; Conservative 94; Mismatches 274; Indels 213; Gaps 31;  Qy 7 IIWNALNAWWAVSELTRNHTKRASATVATAVLATLEATVQASTTDDDDLYLE 60 1:
Db 1003 F	1, J.; Stevens, K.; sila enterica serov se	

	1375 VAIGSGSIAAADNSVALGŢGSVATĒENTISVGSSTNORRITINVAAGKNATDAVNVAQLKS 451 SVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITINVAAGKNATDAVNVAQLKS 451 SVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITINVAAGKNATDAVNVAQLKS 51 SSEAGGVRYDTKADGSIDYSNITLGGGNGG-TTRISNVSAGVNNNDVVNYAQLKĢSVQĒTK 52 SEAGGVRYDTKADGSIDYSNITLGGGNGG-TTRISNVSAGVNNNDVVNYAQLKĢSVQĒTK 53 SEAGGVRYDTKADGSIDYSNITLGGGNGG-TTRISNVSAGVNNNDVVNYAQLKĢSVQĒTK 54 QYTDQRMVEMDNKLSKTĒSKLSGGIASAMAMTGLPQAYTPGASMASIGGGTYNGĒSAVAL 55 QYSSISDGGNWITKGTASGNSRGHFGASASVGVOM 594	Db 1  RESULT AH0110 PLOBABO C; Speac C; Spec C; Date C; Acc C; M; Paritl II, M. A; Titl A; Refe A; Stac A; Stac A; Stac A; Stac A; Stac A; Stac	A; Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175 C; Genetics: A; Gene: YP00902 A; Genetics: A; Gene: YP00902 A; Genetics: A; Gene: YP00902  Query Match Best Local Similarity 25.0%; Pred. No. 1.7e-09; Matches 132; Conservative 73; Mismatches 209; Indels 113; Gaps 21; Qy 99 LTAGTITLKAGDNLKIKQNTNENTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNIT 158
Db 1091 VAIGOGSYSDVDTGIALGSSSVSSRVIAKGSRDTSITENGVVIGYDTTDGELLGALSIGD 1150  Qy 220VLNAGMNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGK 270  1151 DGKYROIINVADGSEAHDAVT-VRQLQNAIGAVATTPTKYFHANSTEEDSLAV 1202  Qy 271 -RTEVKIGAKTSVIKEKDGKLYTGKDKGENDSSTDKGEGLYTAKE 314  1	ACYNNNDVVNY. LPCKSMMAIGG. 1   1   1   1   1   PGASMASIGG	lessingspies	Query Match       12.2%; Score 368.5; DB 2; Length 1588;         Best Local Similarity       23.0%; Pred. No. 7.4e-11;         Matches 174; Conservative 94; Mismatches 274; Indels 213; Gaps 31;         Qy       7 IIWNSALNAWVASELTRNHTKRASATVATALLEATVQASTTDDDDLYLE 60         1:

	Riley, M.; Cc PID:91788309; 28;	OY 53 DDDLYLEPVORTAVVLSRSDKGGTGEKEVTEDSNWGV DD 64SPAMVTASKVMVAHVDSQVNRTADRIPTGDGSELMTHMALDWKFEPFGNNSIA
OY 217 VKDVLNAGWNIKGVKPGTTASDNVDEVRINDEVERSADTKTTTVNVESKDNGKRT 272  Db 314 MASIANGG-GVKYPHANSTOPDSVASGTNSVALGPASLASGNAALASG 360  QY 273EVRIGAKTSVIKEKDGKLVTGKDKGENDSSTDKGEGIVTAKEVIDAVNKAGWRMKTTT 330  Bb 361 AGAVAIGDGAAASADGSVAIGOGSGNGRGVENYIGKYSNASTT 404  QY 331 ANGGTGOADKFETYTSGTNVTFASGKGTTATVSKDDGNITVMYDDVNGGALNVNOLQNS 390  SI	RESULT 10  G64964  Hypotherical protein b2000 - Escherichia coli C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Feb-2001 R: Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Science 277, 1453-1462, 1997 A.Title: The complete genome sequence of Escherichia coli K-12. A.Rocession: 664964 A.Status: nuclect acid sequence not shown; translation not shown A.Status: nuclect acid sequence not shown; translation not shown A.Residues: 11091 CBLAT> A.Experimental source: strain K-12, substrain MG1655 A.Experimental source: strain K-12, substrain MG1655 C;Reywords: nuclectide binding; P-loop F;683-690/Region: nuclectide-binding motif A (P-loop) Cuery Match Best Local Smilarity 22.6%; Pred. No. 8.3e-05; Matches 141; Conservative 64; Mismatches 215; Indels 204; Gaps Cy INMKIYRIINNSALNAWAVSELTRHIFKASATVATLATLATVOASTTDDDLYLE 60 INMKIYRIINNSALNAWAVSELTRHIFKASATVATLATLATTCATTLATGONLKIKGUTNE 120 Db 57 LNTCYRLWNHHMTGAFVVASELTRHIFKASATVATCATTLATGONLKIKGUTNE 120 Db 111 P	Db 188 AGG-GOSLQGRAVNTTLNGGEQWMHEGAIATGTVINDK

	92YFDKKGVLTAGTITLKAGDNLKIKONTNENTNASSFTYSLKKDLTD 137 	Db 752 TTKLTNAASVLTLTNAANAVLTGAIDNTTGGDNVGVLNLNGALSQVTGD- 799 Ov 178 TVHINGTGGGT TPATTINTGATTANDAV
138	LTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVHLNGIGSTLTDTLLNTGA 197  :-	1/8 IVHLNOIGSTILTDILLDHIGGTINVINDIVTUDERKAASKAVKUNAUWNIKVUKEGET   1   1   1   1   1   1   1   1   1
198	TTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADT - 256	QY 235 TASDNVDFVRTYDTVBFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGK 289            : : :         : :         Db 854 TGGDNVGVLNLNGALSQVTGDIGNTNSLAT-ISVGAGTATLGGAVIKATTTK 904
257	KTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKD	QY 290 L
296	-KGENDSSTDKGEGLVTAKEVIDAVNKAGWRWKTTTANGQTGQADKFET - I	OY 310 VTAKEVIDAVNKAGWRWKTTTANGOTGQADKFETVTSGTNVTFASGKGTTATV 362
344	V-TSGTNVTFASGKGTTAT-VSKDDGGNITVMYDVNGDALNVNQLQNSGMNLD	QY 363 SKDDQGNITVMYDVNVGDALNVNQLQNSGNVDSKAVAGSSGKVISGNVSPSKGKMDETV 422  DS 1023GNTNALATVNVGAGLLQVQGGVVKANTINLTDNASÄVTFTNPVVVTGAIDNTG 1075
396	SKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVS	OY 423 NINAGNNIEITRNGKNIDIATSMTPOFSSVSLGAGADAPTLSVDDEG 469
454	LGAGADAPTLSVDDEGALNVGSKD-ANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLN	OY 470 ALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIA 525  1
511	NHIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIG	QY 526 QAIATAGL-VQAYLPGKSMMAIGGGTYRGEAGYAIGY 561  :     ::     :     :   Db 1170 NALATVNVGAGITLQAGGSLAANNIDFGARSTLEFNGPLDGGGKAIPYYFK 1220
548	GGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGA-SASVGY E	Qy 562 SSISDGGNWIIKGTASGNSRGHFGASASVG 591 : ::     :
RESULT 12 A41477 190K surfa	2 sce antigen precursor - Rickettsia rickettsii	RESULT 13 H83135 probable adhesin PA4082 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa
cles; e: 16 essic ersor t. In	C;Species: McKettsia rickettsii C;Date: 16-Sep.1992 #sequence_revision 16-Sep-1992 #text_change 08-Oct-1999 C;Accession: A41477 R;Anderson, B.E.; McDonald, G.A.; Jones, D.C.; Regnery, R.L. Infect. Immun. 58, 2760-2769, 1990	C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: H83135 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lorv, S.; Olson, M.V.
erencession	A;Title: A protective protein antigen of Rickettsia rickettsii has tandemly repeated, ne A;Reference number: A41477; MUID:90354033 A;Accession: A41477 A A;Accession: A41477 A A;Accession: A41477 A A;Accession: A41477 A A;Molecule type: DNA	Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A;Reference number: A82950; MUID:20437337 A;Arcession: H83135
idue ss-r e: t word	A; Residues: 1-2249 <and> A; Residues: 1-2249 <and> A; Cross-references: GB:M31227; NID:g152465; PIDN:AAA26380.1; PID:g152466 A; Note: the authors translated the codon GAT for residue 430 as G1y, and CAA for residue C; Reywords: surface antigen; tandem repeat status predicted <sigu> F;1-20/Domain: signal sequence (uncleaved) #status predicted <sigu></sigu></sigu></and></and>	A; Status: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-1018 <sto> A; Cross-treferences: GB:AE004824; GB:AE004091; NID:g9950277; PIDN:AAG07469.1; GSPDB:GN A; Experimental source: strain PAO1</sto>
ry M	Query Match       7.4%; Score 224; DB 2; Length 2249;         Best Local Similarity       24.2%; Pred; No. 0.0021;	C;Genetics: A;Gene: PA4082
Matches 13	es 171; Conservative 73; Mismatches 256; Indels 206; Gaps 34; 13 LNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLEPVQRT 65	Query Match 7.4%; Score 222; DB 2; Length 1018; Best Local Similarity 22.5%; Pred. No. 0.00097; Matches 148; Conservative 82; Mismatches 233; Indels 196; Gaps 28;
640	640 INLNGALSOVTGDIGNTNSLATISVGAGTATLGGAVIKATTTKITNAVSAVKFTNPVVVT 699 66 AVVISPRSDKRGTGRKEVTEDSNMCVYDNKKGVITAGTITIKAGDNIKIKON 117	Qy I MMKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60
700	GAIDSTGNANNGIVTFTGNSTVTGDIGNTNALATVNVGAGTATLGGAVIKAT 751	61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE
118	TNENTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDT 177	Db 55 PSGGTVVGGSANGEIHLSGGNSLSVNQKVDK 85

QY         236 ASDNVDEVRTYDTVEELSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEK         286           Db         938 FKJIDNSKNLSITTNSSSTYRFIISGNITNRNGDLNITNEGSDTEMOIGGDVSOK         992           QY         287 DGKLVTGKDK	1152 GTTINATTGNVEITAQTGSILGGIESSGSVTLTATEGALVSNISGNTVTVTA 492 KEGDVTNVAOLKGV-AONLNNHIDNVDGNARAGIAOAIATAGLVQAYLPGKSMAAIGG 1206 NSGALTTAGSTIKGTESVTTSSOSGIGGTISGGTVEVKATESLTTGSNSKIKA 549 GTYRCEAGYAIGYSSISDGGWMIKGTASGRS 540 GTYRCEAGYAIGYSISDGGWMIKGTASGNS 580 1	RESULT 15 S28634 additional and precursor - Escherichia coli plasmid piB6 C.Species: Escherichia coli C.Date: 17-Apr.1993 #sequence_revision 17-Apr.1993 #text_change 08-Oct.1999 C.Accession: \$28634; \$22660; \$28881; \$27657 C.Accession: \$28634; \$22660; \$28881; \$27657 R.Benz, I. R.Benz, I. R.Benz, I. R.Berz, I	A; Wolecule type: protein A; Wolecule type: protein A; Wolecule type: protein A; Residues: 50.56 (4813) A; Experimental source: strain 2787 B; Suhr, M.; Benz, I.; Schmidt, M.A. Mol. Microbiol. 22, 31.42, 1996 A; Title: Processing of the AIDA-I precursor: removal of AIDA and evidence for the out A; Accession: \$72657; MUID: 97055419 A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule type: Drotein A; Experimental source: DAEC strain 2787 C; Genetics: all 7-856 <suh> A; Experimental source: DAEC strain 2787 C; Genetics: membrane protein C; Keywords: membrane protein F; 1-49/Domain: signal sequence #status predicted <sig> F; 50-1286/Product: adhesin AIDA-I #status predicted <mat> Cquery Match 7.3%; Score 219; DB 2; Length 1286;</mat></sig></suh>
21 -NTHASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGD 176	1	Qy 477DANKPURITNUAPGUKEGDYINVAQLKGVAQNLNHID 514  bb 450 GGAGSALAMDAGEGHRVNGTASVSLAGANATYSGGYYTTVQNIAQLINKNLDG-LY 508  QY 515 NVDGNARAGEHRANDGTARAGUQAYLPGKSMMAIGG-GTYRGEAGYALGYSSISDGG 568  EDD 509 VLGGNILGGSYYCTALQSIGGPAGVFSGTLDGLGNSIGNLSISNTG 554  RESULT 14  A43855  High-molecular-weight surface-exposed protein HWW1 - Haemophilus influenzae C; Species: Haemophilus influenzae C; Species: Haemophilus influenzae C; Species: Haemophilus influenzae C; Species: LO-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C; Accession: A43855  R; Barenkamp, S.J; Leininger, E. Infect. Immun. 60, 1302-1313, 1992 A; Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Ha A; Reference number: A43855; MUID:92192797 A; Accession: A43855 A; Access	Anote: sequence inconsistent with the nucleotide translation A, Note: sequence extracted from NCBI backbone (NCBIN:89235, NCBIP:89239)  Query Match Best Local Similarity 22.7%; Pred. No. 0.0021; Matches 130; Conservative 88; Mismatches 210; Indels 144; Gaps 30;  Qy 98 VLTAGTITLKAGDNLKIKONTNENTNASSFTYSLKKDLTDLTSVGTEKLSF 148

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30;
                                                                                                                                                                                                                                                                                                                               133 ----KDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVHLN----- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 NIKGSQI-----VNSEGTAINTLVSDGGYQHIRNGGIASGTIVNQSGYVNISSGGY 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 AESTIINSGGTLRVLSDGYARGTILNNSGRENVSNGGVSYNAMINTGGNQYIYSDGEATA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398 AVAGSSG--KVISGNVSPSKGKMDETVNINAGN---NIEITRNGKNI------DIA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:: | : || : || 496 TAVWSMFPGTASGA------NVNLSGRLNAFAGNVVGTILNQEGRQYVYSGATATSTVG 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   475 SKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARA-----GIAQAIA 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549 NNEGREYV----LSGGITDGTVLNSGGLQAVSSG------GKASATVINEGGAQFVY 595
                                                                                                                                                                                                                                           112 L------ 132
                                                                                                                                                                                                                                                                          167 GGITDSTNISSGGQRVSSGGVASNTINS-----SGAQNILSEEGAISTHISSGGNQYI 221
                                                                                                                                                                                                                                                                                                                                                                                                                      GIGSTLIDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 VRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGENDSS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 NSGVQTV-FAGATVTDTTVN--SGGNQNISSGGIVSETTVNVSGTQNIXSG---GSALSA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 TDKGEGLVTAKEVIDAVNKAGWRMKTTTANG-----QTGQADKFETVTSGTNVTFASG-- 355
                                                                                                                                                        52 TDDDDLYLEPVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDN 111
                                                                                                                                                                                                 61 TVSSG-----ETQIVYS-----GRGNSNATVNSGGTQIVNNGGKTTATTVNSSGSQN 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443 TSMTPQFSSVSLGAGADAPTLSVDDEGALN-----------VG 474
Best Local Similarity 20.9%; Pred. No. 0.0018;
Matches 146; Conservative 96; Mismatches 256; Indels 202; Gaps
                                                                                                    1 MIKAYSIIWSHSRQAWIVASELARGHGFVLAKNTLLVLAVVSTIGNAFAVNISGTVSSGG 60
                                                                  1 MNKIYRIIWNSALNAWVAVSELTRNH------TKRASATVATA--VLATLLFATVQAST 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530 TAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGN 569
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Search completed: September 5, 2002, 10:24:32 Job time: 239 sec

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us-09-700-293-2.rsp

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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: September 5, 2002, 10:23:53 ; Search time 19.11 Seconds (without alignments) 1203.528 Million cell updates/sec
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Title: US-09-700-293-2
Perfect score: 3019
Sequence: 1 MNKIYRIIWNSALNAWVAVS.....TASGNSRGHFGASASVGYQW 594

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ρt	P39180 escherichia	P15921 rickettsia	Q03155 escherichia		P16466 proteus mir		P33666 escherichia	Q53047 r outer mem		P35827 campylobact	Q52657 rickettsia	P96989 r outer mem			P52143 escherichia		P35825 bacillus st	P14914 rickettsia	P18127 xanthomonas	2		P45355 haemophilus	O06653 r outer mem			_	Q9phw6 campylobact		rb65	5 chlamydia	5828	6682	Q9zltl helicobacte
SUMMARIES	AG43_ECOLI	OMPA_RICRI	AIDA_ECOLI	YDEK_ECOLI	HLYA_PROMI	HLYA_SERMA	YDBA_ECOLI	OMPB_RICRI	BIGA_SALTY	SLAP_CAMFE	OMPA_RICCN	OMPB_RICTY	OMPB_RICCN	WAPA_BACSU	YPJA_ECOLI	YMJB_CAEEL	SLAP_BACST	120K_RICRI	ICEN_XANCT	FHAB_BORPE	APU_THETU	HXA3_HAEIN	OMPB_RICJA	PMPC_CHLTR	OMPB_RICPR	HPI2_DEIRA	FLID_CAMJE	HXA2_HAEIN	PM10_CHLPN	Y741_CHLMU	SLAP_CAUCR	PMP6_CHLPN	CAGA_HELPJ
08	<u>:</u> -	٦	٦	<b>~</b>	Н	Н	7	٦	П	Н	-	Н	Н	٦	Н	Н	-	Н	-	7	-	-1	Н	Н	-	Н	-	Н	H	Н	<del></del> i	П	Н
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% Query Match	ļ &			7.2	6.8	6.7	9.9			6.4	6.4	6.4	6.4	6.3	6.2	9	5.8	5.7	5.7	5.7	5.7	2.6	5.6	2.6	5.5	5.5	5.5	5.5	5.5	5.5	5.4	5.4	5.4
Score	244	224	219	216.5	204.5	203	198	195	195	194.5	193	192.5	192.5	190	187	180.5	176	173	172.5	172.5	171.5	170.5	170.5	169	167	165.5	165	165	165	165	164.5	9	162.5
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P38058 clostridium P37710 enterococcu	Q48253 helicobacte Q61687 mus musculu Q09624 caenorhabdi	Q08860 shigella fl Q48258 helicobacte	P04949 escherichia P18494 saccharomyc Q01837 listeria iv	P94217 bacillus an P16271 lactococcus
CBPA_CLOCL ALYS_ENTFA	VAC3_HELPY ATRX_MOUSE YS89_CAEEL	FLIC_SHIFL VAC4_HELPY	FLIC_ECOLI GLN3_YEAST P60_LISIV	SLA2_BACAN P1P_LACLC
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## ALIGNMENTS

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                                         229 TANTTVVYAGGDQTVHGH---ALDTTLNGGYQYVHNGGTASDTV--VNSDGWQIVKNGGV 283
                  121 NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH 180
                                                                                                                                                                                                  177 --VKPGTVATDIV--VNTGAEGGPDAENGDTGQFVRGDAVRTTIN----KNGRQIVRAEG 228
                                                                                                                                                                                                                                                                                                          327 -KTTTANGQTGQADKFETVTSGTNVTFASG----KGTTATVSKDDQGNITVMYDVNVGDA 381
                                                                                                                                                                                                                                                                                                                                          284 AGNTTVN-QKGRL-QVDAGGTATNVTLKQGGALVTSTAATVT------323
                                                                                                                                                                                                                                                                                                                                                                               382 LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDI 441
                                                                                                                                                                                                                                                                                                                                                                                                                 324 -GINRL-----LENGGRLDV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 ATSMTPQFSSVSLGA-----GADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496 VTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEA 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412 ADALMLEKGSSFTLN-----AGDTATDTT-------VNGGLFTARG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pl594.7.
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1991 (Rel. 40, Last annotation update)
01-407.2001 (Rel. 40, Last annotation update)
01-407.
                                                                                         181 LNGIGSTL----IDTLLNTG------ATTNVTNDNVTDDEKKRAASVKDVLNAGWNI
                                                                                                                                                                228 KGVKPGTTASDNVDFVRT-----YDTVEFLSADTKTTTVNVESKDNGKRTEVKIG
                                                                                                                                                                                                                                     278 -AKTSVIKEKDGKLVTGKDKGENDSSTDKGEGLV----TAKEVIDAVNKAGWRM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                    136 AGG-GOSLOGRAVNTTLNGGEQWMHEGAIATGTVINDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 2249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              556 GYAIGYSSISDGGNWIIKGTASGN 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 446 GTLAGTTTLNNGAILTLSGKTVNN 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90354033; PubMed-2117568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane protein A partigen) (rOmpA) (rOmp A).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                            FEMS Microbiol. Lett. 149:115-120(1997).
-i- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
8.1%; Score 244; DB 1; Length 1039;
Best Local Similarity 22.6%; Pred. No. 4.6e.05;
Matches 141; Conservative 64; Mismatches 215; Indels 204; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTIGUE 43 BETA CHALIN.

K -> N (IN STRAIN ML 308-225).

T -> K (IN STRAIN ML 308-225).

T -> K (IN STRAIN ML 308-225).

Y -> E (IN STRAIN ML 308-225).

ATN -> STI (IN STRAIN ML 308-225).

ATN -> STI (IN STRAIN ML 308-225).

A -> T (IN STRAIN ML 308-225).

A -> T (IN STRAIN ML 308-225).

E -> V (IN STRAIN ML 308-225).

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C -> T (IN STRAIN ML 308-225).

C -> T (IN STRAIN ML 308-225).

E TV -> TTT (IN REF. 5).

ETV -> TTT (IN REF. 5).
                                                                  MEDLINE-97257509; PubMed-9103983; Henderson.1.R., Meehan M., Owen P.; Antigen 43, a phase-variable bipartite outer membrane protein, determines colony morphology and autoaggregation in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P----TVNGGTLANHDNQIVFGTTNG 82
                                                                                                                                                                                              FUNCTION AS AN ADHESIN.
SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
                                                                                                                                                                                                                                                                     -i- SUBCELLUIAR LOCATION: OUTER MEMBRANE ASSOCIATED.
-i- SIMILARITY: TO ADHESIN ALDI-I AND TO BORDETELLA PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTIGEN 43 ALPHA CHAIN.
ANTIGEN 43 BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000291; AAC75061.1; ALT_INIT.
EMBL; D90838; BAA51825.1; ALT_INIT.
EMBL; U74429; AAB47862.1; ALT_INIT.
EMBL; U74429; AAB47869.1; -1.
ECOGENE: EG12686; FIL.
OULGE MEMDIANE; SIGNAI; COMPLETE Protecome.
in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106841 MW;
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551
1039
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1039 AA;
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CONFLICT
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34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GNTNALATVNVGAGL--LQVQGGVVKANTINLTDNASAVTFTNPVVVTGAIDNTG 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NANNGIVTFTGNSTVTGNVGN-----TNALATVNVGAGLLQVQGGVVKANTINLTDNA 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-----AVTFTN--PVVVTGAIDNTG-----NANNGIVTFTGNSTVTGDIGNT 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1170 NALATVNVGAGITLQA---GGSLAANNIDFGARSTLEFNGPLDGG-----GKAIPYYFK 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----VTGKDKGENDSSTDKGEGL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 VTA-----KEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NINAG-----ADAPTLSVDDEG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVVLSFRSDKEG----TGEKEVTEDSNWGVYFDKKGVLT----AGTITLKAGDNLKIKQN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             700 GAIDSTGNANNGIVTFTGNSTVTGDIG-----NTNALATVNVGAGTATL---GGAVIKAT 751
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  LNAWVAVSELTRN--HTKRASATVATAVLATLLFATVQASTTDDDDL----YLEPVQRT 65
                                                                                                                                                                                                                                                                                                                                                                                                                 905 LINAASVLTLINANAVLIGAIDNTIGGDNVGVLNLNGALSQVIG-DIGNINSLATISVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARA----GIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAIAT----AGL-VQAYLPGKSMMA-------IGGGTYRGEAGYAIGY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 TNENTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 752 TTKLTNAASVL----TLTNANAVLTGAIDNTTGGDNVGV-----LNLNGALSQVTGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 TVHLNGIGSTLTDTLLNTGATTNVTNDNV---TDDEKKRAASVKDVLNAGWNIKGVKPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----IGNTNSLATISVGAGTATLGGAVIKATTTKLTNAASVLTLTNANAVLTGAVDNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 TASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKT----SVIKEKDGK
                                                                                                                                                                                                                                                                                                                                            7.4%; Score 224; DB 1; Length 2249; 24.2%; Pred. No. 0.0011; ive 73; Mismatches 256; Indels 206;
                                                                                        OUTER MEMBRANE PROTEIN A.
13 X APPROXIMATE TANDEM REPEATS.
                                                              wall; S-layer; Glycoprotein. POTENTIAL.
                                                                                                                                                                                                                                                                                                       A9D6646C089DF087 CRC64;
                                                                                                                                                                                                                                                                                            TYPE I (INCOMPLETE)
                                                                                                                  A (TYPE I).
B (TYPE II).
C (TYPE II).
E (TYPE II).
E (TYPE II).
G (TYPE II).
I (TYPE II).
I (TYPE II).
I (TYPE II).
I (TYPE II).
K (TYPE II).
                                                                                                                                                                                                                                                                HI.
                                                                                                                                                                                                                                                                (TYPE
                       PIR; A41477; A41477.
InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
                                                                                                                                                                                                                                                                                                        MΜ
                                                            Antigen; Repeat; Signal; Cell SIGNAL 1 28
                                                                                                                                                                                                                                                                                                        224333
                                                                                                                                                                                                                                                                                                                                                          Local Similarity 24.2%
les 171; Conservative
           EMBL; M31227; AAA26380.1;
                                                                                        2249
1180
                                                                                                                                                                                                                                                                           1165
                                                                                                                                                                                                                                                                1022 109
1094 116
1166 118
2249 AA;
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212
212
287
359
431
506
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                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDDDDLYLEPVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TVSSG-----ETQIVYS-----GRGNSNATVNSGGTQIVNNGGKTTATTVNSSGSQN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L------132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 VGTSGATISTIVNSGGIQRVSSGGVASATNLSGGAQNI-YNLGHASNTVIFSGGNQTIFS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVHLN----- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGITDSTNISSGGQQRVSSGGVASNTINS----SGAQNILSEEGAISTHISSGGNQYI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNKAYSIIWSHSRQAMIVASELARGHGFVLAKNTLLVLAVVSTIGNAFAVNISGTVSSGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNKIYRIIWNSALNAWVAVSELTRNH-----TKRASATVATA--VLATLLFATVQAST 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthesized via a precursor molecule.";
Mol. Microbiol. 6:1539-1546(1992)
-i- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 219; DB 1; Length 1286;
Pred. No. 0.001;
6; Mismatches 256; Indels 202;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
STRAIN=2787 (0126:H27);
MEDLINE=92226638; PubMed=1625582;
MEDZINE SCAMMICH M.A.;
"AIDA I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escherichia coli strain 2787 (0126:H27), is
                      1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;
GTASGNSRGH- - - FGASASVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S28634; S28634.
Cell adhesion; Signal; Outer membrane; Plasmid.
                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADHESIN AIDA-I.
                                                                                                                          PRT; 1286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.3%;
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                                                                                                                                                                                                                  Adhesin aidA-I precursor.
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                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO EPITHELIAL CELLS.
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562 SSISDGGNWIIK-
                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562;
                                                                                                                                                                                                                                                                           Plasmid pIB6
                                                                                                                                                                                                                                                                                                         Escherichia.
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Best Local Simi
Matches 146;
                                                                                                                          AIDA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                      RESULT 3
AIDA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1153:345-347(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PVQRTAVVLSFRSDKEGTGEKEVTEDS----NWGVYFDK--KGVLTAGTITLKAGDNLKI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 ----TLGVLLALSGSASGASLEVDNDOITNIDTDVAYDAYLVGWYGTGVLNILAGGNASL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 KQNTNENTNASSFTYSLKKDLTDLTSV--GTEKLSFSANSNK-VNI-TSDTKGLNFAKK- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 -----TITITSVIGANEDSEGTVNVLGGTWRLXDSGNNARPLNVGQSGTGTLNIKQKG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 IVAIL-----GYQAGSNGQ--------VVVEKGGEWLIKNNDS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 RTEVKIGAKTSVIKEKDGKLVTGKDKGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SIEFQIG-----IGT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 ANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALN--VNQLQ 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 LNVQ--DQDSVITVRRLYNGYFGNG---TVNISNNGLINNKEYSLVGVQDGSHGVVNVTD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 NSGWNL-----DSKAVAGSSGKVISGNVSPSKGKMDETVNINAGN---- 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60
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                                                                        (Potential).
--- SIMILARITY: TO E.COLI YFAL.
--- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS ISP42 AND MOM38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 -----TAETNGDTTVHLNGIGSTLTDTLLNTGA----TTNVTNDNVTDDEKKRAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 HVDGGYLRLGSSTGGVGTVNVEGEDSVLTTELFEIGSYGTGSLNIT-----DKGYVTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 23.1%; Pred. No. 0.0014;
Matches 150; Conservative 75; Mismatches 260; Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%; Score 216.5; DB 1; Length 1325; 33.1%; Pred: No. 0.0014;
                                                                                                                                                                                                -!- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL LIPOPROTEIN YDEK.
N-ACYL DIGLYCERIDE (POTENTIAL).
N -> K (IN REF. 3).
M -> S (IN REF. 3).
WW: 26A3A066FA19AD7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1317 1317 M -
1325 AA; 136514 MW;
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A Note that Table Tabl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Outer membrane.

MAY BE RESPONSIBLE FOR PORE FORMATION.
SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 ------ KONTNENTNASSFTYSLKK------DLTDLT----- 139
                                                       505
388 DKNSVITNLGTNLGYDGHGEMNISNQGLVVSNGGSSLGYGETGVGNVSITTGGMWEVNKN 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 LTKTELKGKNIT-----LVASSHNQIKASDLMGDDITLQGADLTI------DGKQLQQK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GVYFDKKG-----VLTAGTITL-----KAGDNLKI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETDIDNRWFYSWKYDVTKEKEQIQQIGSQIDAKNNATLTATKGDVTLDAAKINAGNNLAI 424
                                                                                                                                                                                                                                                                                                                                                                                                                        hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB)."; J. Bacteriol. 172:1206-1216(1990).

-i- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 LTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLEPVQRTAVVLSFRSDKEGTGEK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINENT
CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
FILLING OF THEFORMTON WITH THE BRYTHROCYTE MEMBRANE. HPMA
                                                                                                                                                                                                                                                                                                                                                                                         Uphoff T.S., Welch R.A.;
"Nucleotide sequencing of the Proteus mirabilis calcium-independent
                                           448 VYTTIGVAGVGNLNISDGG--KFVSQNITFLGDKASGIGTLNLMDATSSFDTVGINVGNF
                           VRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLP--
                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. REQUIRES HPMB FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.8%; Score 204.5; DB 1; Length 1577; 22.6%; Pred. No. 0.0066; Live 76; Mismatches 257; Indels 177;
                                                                                 540 GKSMMAIGGGTYRGEAGYAI-----GYSSISDGGNWIIKGTASGNSR 581
                                                                                                   30 1577 HEMOLYSIN.
1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;
                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                   1577 AA
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A35140; A35140.
Hemolysis; Toxin; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ISOLATE 477-12;
MEDLINE=90170827; PubMed=2407716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M30186; AAA25657.1; -.
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                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                       Hemolysin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 EVTEDSNW----
                                                                                                                                                                                                                                                                                 Proteus mirabilis
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 149;
                                                                                                                                                                                 HLYA_PROMI
P16466;
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                                                                                                                                                                  HLYA_PROMI
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                                                                                                                                                                                                                                                                                                                                     296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 ENDSSTD----KGEGLVT------AKEVIDAVNKAGWRMKTTTANGQTGQADK 340
                                                                                                               -SVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVHLN-----GIGSTLTDTLL 193
                                                                                                                                                                                185 GSITAQGAKLHANENVLVNAKDNINLNVQK----TNNDKTVTDNHVMWGGIGGGQNKNNN 540
                                                                                                                                                                                                                                                                194 NIGATINVINDINVIDDEKKRAASVKDVLNAGWNIKG-----VKPGTIASDNVDFVRIYDT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597 ISKIDERTGTAFNITKSSHKNETNKQTSTGSELISDAQLTVVSGNDVNVIGSLIKSADKL 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 FETVTSGTNVTFASGKGTTATVS--KDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 A-----SKDANKPVR----IT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  830 ASHHVEGRYQESGENIQHLAVNDSETSKTDSLNVGIDVGVNLDYSGVTKPVKKAIEDGVN 889
717 ANSTISGANVDLQANKDVTFAGSDLKTTAGNASITGD-NVAFVSTENKKQTD--NTDTTI 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 VAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN-GKNIDIATSMTPQFSSVSLGAG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         890 TTKPG-NNTDLTKKVTARDAIANLANLENDROGVEVGIKGGGSQOSQTDSQAVSTS 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poole K., Schiebel E., Braun V.; "Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 170:3177-3188(1988).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                     541 NQQQVSHAT--QLTADGQLLLAADNNVNITGSQVKGNQGAFVK--TTQGDVVIDNALSET
                                                                                                                                                                                                                                                                                                                                                                                                              249 VEFLSAD-----TKTTTVNVESKDNGKRTEVKIGAKTSVIKEKD----GKLVTGKDKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      774 SGGFS---YTGGVDKVGSKADFQYD-KQHTQTEVTKNRGSQTEVAGDLTITANKDLLHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486 NVAPGVKEGDVTNVAQLKGVAQNLNN--HIDNVDGNARAGI------AQAIATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serratia marcescens.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REQUIRES SHLB FUNCTION.
SUBCELLULAR LOCATION: Outer membrane.
SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPWA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 14, Last sequence update) (Rel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poole K., Schiebel
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01-NOV-1990
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P15320;
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                                                                                                               140
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151; Conservative
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CONFLICT 489 489
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 151; Conserv
             Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
          δy
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                                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                                                                                                                                               471 WSNSDESESIKASELRSEGELTIKAGRNVSTQ-----GAKVHAQRDLTIDADNQIQVGV 524
                                                                                                                                                                                                                                                                                                                                                                                                                                           525 QKTANAKAVRDDK-----TSWG----TSWG----GIGGGDN-KNNSNRREIS 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       988 ODEOSRDIRGSAGVRVYITIGSDLIVDAKGEGGIORSNSSASQAVIGSIDAANGINVNVK 1047
                                                                                                                                                                                                                                                                                                                                                                                                63 QRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNENT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 603 NALSTIVDKIDARIGIAFNIISSSHKADNSYQSSIASEL------KSDINLT 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 FVRTYDTVEF-----ESKDNG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 KRTEVKI-----GAKTSVIKEKDGKLVTG--KDKGENDSS-----TDKGEGLVTAKEV 315
                                                                                                                                                                                                           Query Match 6.7%; Score 203; DB 1; Length 1608;
Best Local Similarity 22.9%; Pred. No. 0.008;
Matches 156; Conservative 82; Mismatches 259; Indels 184; Gaps
                                                                                                                                                                                                                                                                                                    9 W-NSALNAWVAVSELTRNH--TKRASATVATAVLATLLFATVQAS---TTDDDDLYLEPV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 NASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNIT-SDTKGLNFAKKTAETNGDTTVHL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 NAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEG------ALNVGSKD 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       881 ------GANVDYSAVTRPVERAVGKAAKLDA-TGVINDIGGIGAPNVGLDIGAQG 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 ANKPVRITN---VAPGVKEGDV-----TNVAQLKGVAQNLNNHIDNVDGNARA 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           929 GSSEKRSSSSQAVVSSVQAGSIDINAKGEVRDQGTQYQASKG-AVNLTADSHRSEAAANR 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         523 GIAQAIATAGL--VQAYLPGKSMMAIG----GGTYRGEAGYAIGYSSISDGGNW----- 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          769 SFLAADDKTASNTEQTKIGGGFYYTGGIDK---LGSGVEAGYENNK-TQAQSSKAITSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   709 YRAGLRIEHTRDSEKTTRTENSASSLSGGSVKLKAEKDVTFSGSKLVADKGDASVSGNKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 --IDAVNKAGWRMKTTTANG---QTGQADKFETVTSGTNVTFASGKGTTATVSK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 DDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           825 DVKGNLT----INARDKLTQQGAQHSVGGAYQENAAGVDHLAAADTASTTTTKTDVGVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                 31 1608 HEMOLYSIN.
1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDBA_ECOLI STANDARD; PRT; 2003 AA. P3366; P76087; P76089; P76088; P76085; P76087; P76089; P76081, P76089; P76087; P76089; P76087; P760
                                                        Hemolysis; Toxin; Outer membrane; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1048 KDAIYOGTALNGGRGKTAVNA 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     571 ---IIKGTASGNSRGHFGASA 588
                        EMBL; M22618; AAA50323.1; -. PIR; A28182; A28182.
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                                                                                                                                          SEQUENCE
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TD YDBA_EC
AC P33666
DT 01-FEB
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DT 16-OCT
DE HYPOTH
GN YDBA O
GN ESCHOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitakawa M., Kasai H., Mashimoto K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Mokade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takkada J., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Corresponding to the Escherichia coli K-12 genome Corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 DKEGTGEKEVTEDSNWGVYFDK-KGVLTA------GTITLKAGDNLKIKQNTNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 DDTPTPPKPVSFNND--VILDKTEKTLTIRDSVFTYTENADGTISLODSNGRKATINIMQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTT-V 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.6%; Score 198; DB 1; Length 2003;
24.7%; Pred. No. 0.018;
Live 74; Mismatches 229; Indels 158; Gaps
SEQUENCE FROM N.A.

STRAINH-MIZ / MG1655;

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Punkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

Mau B., Shao Y.;

"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 ATVATAVLATLLFATVQASTTDD-------DDLYLEPVQRTAVVLSFRS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG (AC P25928).
-1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT BETWEEN AMINO ACIDS 839 AND 840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moszer I., Glaser P., Danchin A.; "Multiple IS Insertion sequences near the replication terminus in Escherichia coli K-12."; Biochimie 73:1361-1374(1991).
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BEBL; AE000237; AAC74487.1; AIT_SEQ.
EMBL; D90778; BAA15099.1; AIT_SEQ.
EMBL; D90778; BAA18880.1; AIT_SEQ.
EMBL; D90779; BAA18881.1; AIT_SEQ.
EMBL; X62680; -; NOT_ANNOTATED_CDS.
ECOGene; EG11307; ydDA.
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12;
MEDLINE=97251357; PubMed=9097039;
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SEQUENCE OF 464-2003 FROM N.A.
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189 IDEANN-TVALE----GVSADGATKWQYNHNGELV-ITGDNATVNNNGKTTVDGKDSTGT 242
                                                                                                        573
                                                                                                                                                                          358 SGGGHGIDITGDSATVDNKGTMTVTDPESIGIQVDGDQAVVNNEG---ESAITNGGTG-- 412
                                                                                                                                                                                                        DKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKA 398
                                                                                                                                                                                                                                                               VAGSSGKVI-SGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMT---PQFSSVSL 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-R;
MEDLINE=92167802; PubMed=1724278;
Gilmore R.D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.;
Gilmore R.D. diodalton outer membrane protein (rOmp B) of Rickettsla
The 120 kilodalton outer membrane protein (rOmp B) of Rickettsla
rickettsli is encoded by an unusually long open reading frame:
                                             292 TGKDKG---ENDSST--DKGEGLVTAKEVID-----AVNKAGWRMKTTTANGQTGQA
                                                                                                                                                                                                                                                                                                                          GAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNH-I
                                                                                                                                                                                                                                                                                                                                                                                                               526 TTVDGKDSTG-TKIAGNIGIVN--LDG-SLTVTGG------AHGVENIGDNGTVNNK
                           HLNG-IGSTLTDTLLNT---GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTT
                                                                                     ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGK---RTEVKIGAKTSVIKEKDGKL-V
                                                                                                                                                                                                                                                                                                                                                     486 GIQIDGDQAIVNNEGEST-----ITNGGTG------TQINGNDATANNSGK
                                                                                                                                                                                                                                                                                                                                                                                    514 DNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia rickettsii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                    ----TQINGDDAT-ANNNGKTTVDGKDSTGT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GTASGNSRGHFG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDIVVSDTGSIG
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ID OMPB_RICRI
AC Q53047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTEDSNWGVYFDK-----KGVL--TAGTITLKAGDNLKIKQNTNENTNASSFTYSLK--K 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 TLT-ITGGGVTNAQAAATKNAQNVVVQFNNGAAIDNNDLKGVGRIDFGAPASTLVFNLAN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDDQGNITVMYDVNVGDALN - - VNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKM - - - 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 ASATVATAVLATLLFATVQ-----ASTTDDDDLYLEPVQRTAVVLSFRSDKEGTGEKE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATIVASFAGSAMGAAIQQNRTTNGAATTVDGAGFDQTAAPANVGVALNA-----V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------DETVNINA-GNNIEITRNGKNI----DIATSMTPQFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 DLTDLTSVGTEKLSFSANSNKVNI-----TSDTKGL------NFAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LLNT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 PTTQKAPLILGDNAVIANGVNGTLNVTNGFIQVSNKSFATVKAINIADGQGIIFNTDANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GATTNVTNDNVTDD----EKKRAASVKDVLNA-GWNIKGVKPGTTASDNVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       543 MMAIGGGTYRGEAGYA-----IGYSSISDGGNWIIKGTASGNSRGHFGASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 KDA SURFACE-EXPOSED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 195; DB 1; Length 1654; Pred. No. 0.02; 93; Mismatches 273; Indels 24
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D7AB70FB7087F618 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 KDA BETA PEPTIDE.
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                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003858; rompA_rompB.
Pfam; PF02708; rompA_rompB; 1.
Antigen; S-layer; Cell wall. 120
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-LT2 / SGSG1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
MEDLINE-21534948; PubMed-11677609;
MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., MCCLelland W., Sanderson R.E., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 173:325-333(1991).
-I- CAUTION: Ref.3 sequence differs from that shown due to frameshifts in positions 414 and 732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91100301; PubMed-1987123; Wu Jr., Slegel L.M., Kreddich N.M.; High-level expression of Escherichia coli NADPH-sulfite reductase: requirement for a cloned cysG plasmid to overcome limiting siroheme
                                                                                                                                  P105-2011

P25927; P25928; 03503;

01-MAY-1092 (Rel. 22, Created)

01-MAR-2002 (Rel. 41, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation update)

Putative surface-exposed virulence protein bigA precursor.

Salmonella typhimurium.

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
PUTATIVE SURFACE-EXPOSED VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                                       Stolli)Kovic I., Valentine P., Heffron F.; "Salmonella typhimurium rhs homolog."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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Vitulence; Repeat; Signal; Complete proteome.
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28 1953 PUTALIVE SURFACE
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PIR; D39200; D39200
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SEQUENCE FROM N.A.
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P25927: D25
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21.7%; Pred. No. 0.025;
tive 81; Mismatches 232; Indels 196; Gaps
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D -> DREDDOVTPEPD (IN REF. 1).
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C -> N (IN REF. 1).
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-FATVQASTIDDDDLYLEPVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 LTADSRTSVNLTATNDTITLTSANAATSVNLKQRQAKDAT-ITSAMQQK--YNNRRNRIA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 NITSDIKGLNFAKKTAETNGDITVHLN-GIGSTLTDIL------LNTGATTNVTND 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540 TTAFNALQSV-----SFGKIGQGGKF-SVKTGTGDDKIEFVGTTLTEGSVIDAP 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAG---SSGKVISGNVSPSKGKMDETVNI 424
                                                                                                                                                                                                                                                                                               Blaser M.J., Gotschlich E.C.;
J. Balol. Chem. 265:13372-19372(1990).

-1. FULCTION: THE S.LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS CRITICAL FOW YINGUENCE.

-1. SUBCELULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 181; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AVLATL 42
                                                 Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 VTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSK--DDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFDSATAKTTSVTASG-----SGKTLVIKGAEVETLVNID-----
                                                                                                                                                                         Blaser M.J., Gotschlich E.C.; "Surface array protein of Campylobacter fetus. Cloning and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J05577; AAA23032.1; -.
Cell wall; S-layer.
SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87; Mismatches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
S-layer protein (Surface array protein) (SAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Score 194.5; DB 23.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVAT-
                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
                                                                                                                                                                                                                         Biol. Chem. 265:14529-14535(1990)
                                                                                                                                      STRAIN=84-32 / 23D;
MEDLINE=90354448; PubMed=2387868;
                                                                                                                                                                                                                                                                                MEDLINE-91035477; PubMed-2229082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 151; Conservative
                                 Campylobacter fetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                    NCBI_TaxID=196;
                                                                      Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial
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STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;

STRAIN=197015921; PubMed-8862558;

MEDLINE=97015921; PubMed-8862558;

"Differentiation of spotted fever group rickettsiae by sequencing and analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein rompA.";

J. Clin. Microbiol. 34:2058-2065(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MAINS /;
MEDLINE-94171067; PubMed-8125327;
Crocquet-Valdes P.A., Weiss K., Walker D.H.;
Crocquet-valdes p.A., Weiss K., Walker D.H.;
"Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Mailsh 7 strain).";
Gene 140:115-119(1994).
                                                                  NKDQVI-----NFTAADAGSVKLITVKLN---DVTALMIVVKIVLDAAAKD------ 690
                                                                                                                                     INVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPGKSMM 544
NAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRI 484
                                                                                                                                                                                                            691 TNIALGTAAADKALV-----IDTGIETLNITSLVKATSPETTANTVNAKLTDVTSI 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the outer surface protein rompa.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).
--- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
--- PTM: GLYCOSYLATED (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q52657; P95591; P95593; P95593; P95594; Q52667; Q52668; Q52669; Q52669; Q52670; Q52670
                                                                                                                                                                                                                                                                                                                           MEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                               545 AIGG------GTYRG-----EAGYAIGYSSISDGGNWIIKGTASGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ρχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Indian tick typhus, MI, Malish 7, and Moroccan; Raoult D., Fournier P.E., Roux V.; "Phylogenetic analysis of spotted fever group rickettsiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mechanisms of evolution in Rickettsia conorii and Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2021 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsia conorii.
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STRAIN-Malish
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KQNTNENT-NASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAET 173
                                                                                                                                                                     599 KATTIKLIDINASAVIFT----NPVVVTGAIDNIGNANNGIVIFTGNS---TVTGNIGNI 650
                                                                                                                                                                                                                               174 NGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       992 KGAIANGNNAILNVNTKLLTAYHLTIGTVAEINIGAGNLFAIDASAGDVTÍLNAQDIHFR 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1052 ALDSALVLSNLTGVGVNNILLAADLVAPGVDEGTVVFDGGVNGLNIGSNVA---GAARNI 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1109 GDVGGNKFNTLLIYNAVTITDDVNLEGIQNVLINNNADFTSSTAFNAGTIQ----- 1159
                                                                                                                                                                                                                                                                            234 TTASDNVDFVRTYDTVEFLSADTKTT----TVNV---ESKDNG---KRTEVKIGAKTSVI 283
                                                                                                                                                                                                                                                                                                                                                                                              284 KEKDGKLVTG----KDKGENDSSTDKGEGLVTAK----EVIDAVNKA-----GWRMKT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                760 TFTNPVVVTGAIDNTGNANNGIATFTGDSTVTGNIGNTNALATVNVGAGLLRVQGGVVKS 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 TTAN----SGTN----VTFAS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  820 NTINLTDNASAVTFTNPVVVTGAIDNTGNANNGIVTFTGDSTVTGNIGNTNALATISVGA 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKGT-----TATVSKDDOGNITVMYDVNVGDALNVNQLQNSGMNLDSKAVAGSSGKV 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --TLSVDDEGALNVGSK------ 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISGNVSPSKGKMDETVNINAGNNIEI--TRNGKNIDIATSMTPQFSSVSLGAGADAP--- 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 -----TNVAQLKGVAQNL 509
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rompb)
antigen) (Clopp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=WILMINGTON.

STRAIN=WILMINGTON.

MEDLINE=94040787; PubMed=8224886;

Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;

"Cloning and sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi.";

[6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiacea; Rickettsieae; Rickettsia.
NCBL_TAXID-785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1160 -INDATYTIDANNGNLNIPAGNIKFAHADAQLILQNSSGNDR 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1645 AA
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             (See http://www.isb-sib.ch/announce/
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R -> H (IN STRAIN INDIAN TICK TYPHUS).
MISSING (IN STRAIN MJ).
WT -> II (IN STRAIN MOROCCAN).
VT -> II (IN STRAIN INDIAN TICK TYPHUS).
D -> A (IN STRAIN INDIAN TICK TYPHUS).
AND MOROCCAN).
N -> H (IN STRAIN MOROCCAN).
M -> I (IN STRAIN MOROCCAN).
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N -> H (IN STRAIN MOROCCAN).

Q -> K (IN REF. 1).

I -> V (IN REF. 1).

V -> I (IN REF. 1).

T -> N (IN REF. 1).

IS -> D (IN REF. 1).

IS -> V (IN REF. 1).

IS -> V (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 VLSFRSDKEGTGEKEVTEDSNWG-VYFDKKGVLTA------GTITLKAG----DNLKI 114
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N -> D (IN REF. 1).

V -> I (IN REF. 1).

N -> D (IN REF. 1).

VN -> IS (IN REF. 1).

LLRVQGGVVKSNTIN -> KATLGGAIIKATTTK (IN
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21.7%; Pred. No. 0.033;
tive 90; Mismatches 269; Indels 238;
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G -> R (IN REF. 1).
MY 327FC42D7CB24668 CRC64;
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Pfam; PF02708; rOmpA_rOmpB: 1.
Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein;
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THR-RICH.
entities requires a license agreement (
or send an email to license@isb-sib.ch)
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DOMAIN
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Stenos J., Walker D.;
"The rickettsial outer membrane protein A and B genes of Rickettsia australis a lotted fever group.";
submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(Tomp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                 |: | |: | ||: | 572
| SIQLDGSAIITGDIGNGAVNAALQDITLANDASKILTLSGANIIGANAGGAIHFQANGG 572
                                                                                                                                                                                                                                                                                                              454 VTNIKAIEVEGAGIVQLSGIHGAELRLGNAGSIFKLA-DGTVINGPVNQNPLVNNNALAA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        573 TIQLTSTQNNILVDFDLDVTTDQTGVVDASSLTNNQTLTINGSIGTIGANTKTLGRFNVG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                524 IAQAIATAGLV-------QAYLPGKSMMAIGGGTYRGEAGYAIGYSSISD 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     633 SSKTILNAGDVAINELVMENDGSVHLTHNTYLITKTINAANQGKIIVAADPINTDTALAD 692
                                --GQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                                                                                                                                                               401 DFGNLAVQIVVPNNKILTGNFIGDA-----KNNG-NTAGVITFNANGTLVSGNTDPNIV 453
                                                                                                                                                                                                                                                   ----KGKMDETVNI--------NAGNNIEITRNGKNIDIATSMTPQFSSVSLGA 456
                                                                                                                                                                                                                                                                                                                                                                   GA---DAPTLSVDD--EGALNVGSKD---ANKPVRITNVAP----GVKEG------ 494
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Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
                                                                356 V-----IQSANAGGQVTFEHLVDVGLGGKTNFKTADSKVITENASFGST-----
                                                                                                                                          DQGNITVMYDVN------VGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPS--
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Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1655 AA
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16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Indian tick typhus, and Malish 7;
MEDLINE=20393643; PubMed=10939649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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MEDLINE=21442074; PubMed=11557893;
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                                IDAVNKAGWRMKTTTANGQT --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia conorii.
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OMPB_RICCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                Hackstadt T. Wesser R., Cieplak W., Peacock M.G.;
Hackstadt T., Wesser R., Cieplak W., Peacock M.G.;
"Evidence for proteolytic cleavage of the 120-kilodalton outer
membrane protein of rickettslae: identification of an avirulent
mutant deficient in processing.";
Infect. Immun. 60:159-165(1992).
-! FUNCTION: THE 120 kpa SURPACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DUBING INFECTION.
-! FUNCTION: THE 32 kpa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
-! SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL SYMMETRY.
-! SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 LGDNAKIVNGANGIL------NITNGFV------KVSDKTFAG--IKTINIG 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LYLEPVOR 64
                                                                      Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sites on CNBr fragments of
the S-layer protein antigens of Rickettsia typhi and Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 NENTNASSFTYSLKKDLTDLTSVGTEKLSFSA----NSNKVNITSDTKGLNFAKKTAET
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32 KDA BETA PEPTIDE.
MEMBRANE ANCHOR (POTENTIAL).
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V -> I (IN REF. 2).
G -> A (IN REF. 2).
G -> S (IN REF. 2).
My. OCB5641C7EB185EE CRC64;
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80; Mismatches 258;
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IDENTIFICATION OF CLEAVAGE SITE.
MEDLINE-92104668; PubMed-1729180;
                                                    PubMed=1370573;
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                                                                                                                                                                                         Mol. Immunol. 29:95-105(1992).
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1645 AA; 169698 M
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Matches 160; Conserv
                          STRAIN-WILMINGTON;
MEDLINE-92114896;
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CHAIN 1
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SEQUENCE FROM N.A.
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                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
SIMILARITY).

FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR EVORTION: THE SIMILARITY).

SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A SLAYER THE HEAGGNAL. SYMBETRY (STMILARITY).

SIMILARITY: BELONGS TO THE RICKETTSTARE OMPANOMPB FAMILY.
                                                                                                                                                                                                                                                          11; Complete proteome.
11; Complete proteome.
32 KDA BETA BERFACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
P -> A (IN STRAIN INDIAN TICK TYPHUS).
K -> N (IN STRAIN INDIAN TICK TYPHUS).
K -> N (IN STRAIN INDIAN TICK TYPHUS).
N -> D (IN STRAIN INDIAN TICK TYPHUS).
N -> D (IN STRAIN INDIAN TICK TYPHUS).
N -> D (IN STRAIN INDIAN TICK TYPHUS).
N -> V (IN STRAIN INDIAN TICK TYPHUS).
R -> L (IN STRAIN INDIAN TICK TYPHUS).
R -> L (IN STRAIN INDIAN TICK TYPHUS).
F -> S (IN REF. 3).
E -> D (IN REF. 3).
C -> S (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 ANAVGOVNFRHIVDVGTDGTTAFKTAASKVAITQNSNFGTTDFGNLAAQIIVPNTMTLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 GWNIKGVKPGTTASDNVDFVRTYD---TVEFLSADTKTTTVN----VESKDNG-----
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                                                                                                                                                                                     EMBL; AEC008659; AAL03623.1; -.
EMBL; AF123721; AAF34124.1; -.
EMBL; AF123726; AAF34129.1; -.
EMBL; AF149110; AAD39533.1; -.
InterPro; IPR003858; rompA_rompB.
Pfam; PF02708; rompA_rompB; 1.
Antigen; S-layer; Cell wall; Complet
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\), 168342 |
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Best Local Similarity 22.49
Matches 149; Conservative
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-1- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).

This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIANE-168 / BGSC1A1;
MEDIANE-95219088; PubMed=7704263;
MEDIANE-95219088 K.I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
"Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome containing the hut and wapa loci.";
Microbiology 141:337-343(1995).
                                   GDVAINELVIGNNGAVQFAHNTYLITRTTNAAGQGKIIFNPVVNNNTTLATGTNLGS-AT
                                                                                                                                    DDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDG-NARAGI
                                                                                                                                                                                               525 AQAIATAGLVQ-----AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTAS
ETVNIN---AGNN--IEITRNGKNIDIATSMTPQ----FSSV----SLGAGADAPTLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-168;
MEDLINE-93302506; PubMed-8316082;
Foster S.J.; analysis of three major wall-associated proteins of "Molecular analysis of three processing of the product of gene encoding a 258 kba precursor two-domain ligand-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
Bacteria, Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID-1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
Wall-associated protein precursor.
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1053 YDENG-HVTSITGPKN--KKV----TYSYENDLLKKVTDT---DGTVTSYDYDSEGRL 1100
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EMBL; AE000350; AAC75695.1; -.
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STRAIN-K12 / MG1655;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                               R EMBL; L05644; AAA22883.1; ...
R EMBL; D31856; BAA06656.1; ...
R EMBL; D31856; BAA06656.1; ...
R EMBL; D39985; BAA06633.1; ...
R EMBL; Z99124; CAB15959.1; ...
R EMBL; Z99124; CAB1593.1; ...
R EMBL; Z99124
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                    1202 GKAT------TYEYNKNDVTK 1238
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                                                                                                                                                                                                                                                                      1145 KTLLM---TQPNGRKVQYGYNEAGNPIQVIDDAEGLKITTNTKYEGNNVVEDVDPNDVGT 1201
                                                                                                                                                                                257 KTTTVNVESKDNGKRTEV---KIGAKTSVIKEKDGKLVTGKDKGENDS-----STDKGE 307
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DNA Res. 4:91-13(1997).
I- SIBGELLULAR LOCATION. Outer membrane (Potential).
I- SIMILARITY: STRONG, TO BORDETELLA PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSV--DDEGALNVGSK 476
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
    ----SDNVDFVRTYDTVEFLSADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacterlaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPJA_ECOLI STANDARD; PRT; 1569 AA. P512143; P76610; P770119; 1569 AJ. D1-COT-1996 (Rel. 34, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-COT-2001 (Rel. 40, Last annotation update) Hypothetical outer membrane protein ypja.
210 EKKRAASVKDVLNAGWNIKGVKPGTTA-----
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us-09-700-293-2.rsp

Search completed: September 5, 2002, 10:31:01 Job time: 428 sec

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Best Local Similarity 100.
Matches 594; Conservative
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Copyright (c) 1993 - 2000 Compugen Ltd
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09jpr7 neisseria m 09jps9 neisseria m 09jps0 neisseria m 09jps neisseria m 09jpd neisseria m 09jqv4 neisseria m 09jqv4 neisseria m 09jps1 paemophilus 09jc3x5 pasteurella 09jc4x rhizobuum m 098h; rhizobuum m 098h; rhizobuum m 09gh; recherichia 09jc4x rhizobuum m 09gh; secherichia 09jc4x santhomonas 09fda0 kanthomonas 09fhuc pseudomonas
                                                                                                                                                                                                                                                                                                                               FTRAIN-EG327;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR157605; AAK68866.1; -.
SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3ABEA2 CRC64;
                                                                                                                                                                                                                                                                                                      Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                            (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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09JPS1
04B152
09F3X6
09F0X6
09F3X5
09F3X5
09F3X7
09BXC7
09BXC7
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       Q9JPS9
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Q93QY2
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Q98JH8
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 Neisseria meningitidis
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Bacteria; Protec
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Q93QY4;
01-DEC-2001 (
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100.0%; Score 3019; DB 2; Length 594; 100.0%; Pred. No. 1.2e-118; Live 0; Mismatches 0; Indels 0

Similarity

PVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQNTNE 120

MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE

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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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STRAIN-813/8B, AND B2232;
STRAIN-813/8B, AND B2232;
PIZZA M., SACHISTO V., Masignani V., Giuliani M.M., Arico' B.,
PIZZA M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
Tidentification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
                                                                            LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
                 LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
                                                          DEVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGEND
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01-OCT-2000 (TIEMBLEG1. 15, Last sequence update).
01-MRK-2001 (TIEMBLEG1. 16, Last annotation update)
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EMBL; AF226369; AAF42518.1; -.
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                                      181 LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
                                                   SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
                                                                                                                                                                                           TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
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97.0%; Pred. No. 8.2e-115;
Live 5; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      09JPS2 PRELIMINARY; PRT; 594 AA.
09JPS2;
01-OGT-2000 (TIEMBLEE]. 15, Created)
01-OGT-2000 (TIEMBLEE]. 15, Last sequence update)
01-MAR-2001 (TIEMBLEE]. 16, Last sequence update)
01-TER MEMBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-NGE31;
MEDLINE-20175756; PubMed-10710308;
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Best Local Similarity 97.04
Matches 576; Conservative
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Neisseria meningitidis.
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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                                                       DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGEND
 NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH
                                           LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
                                                                                                                                    SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226388; AAF42577.1;
EMBL; AF226388; AAF42507.1;
EMBL; AF157604; AAK68865.1;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLRel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN)
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STRAIN-BZ198, AND 297-0;
MEDLINE-20175756; Pubmed-10710308;
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                                 Gaps
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                                                           1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE
                                                                                                                                                                                                                                                                                                           DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGEND
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                                Indels
   Length
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SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
 ; DB 2;
1.3e-112;
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                              Mismatches
Score 2874;
Pred. No. 1.
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95.2%;
                                Conservative
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                 Similarity
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                            568;
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   Query Match
                Sest Local
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                               4; Gaps
                                                      1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60
                                                                       Neisseria meningitidis.
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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STRAIL-2996;
MEDLINE-2015756; PubMed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Pizza M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galcotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                  177 TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
   Length 598;
                             21; Indels
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2001 (TrEMBLrel. 16, Last annotation update)
00TER_MEMBRANE PROTEIN GNA992.
Score 2863; DB 2;
Pred. No. 3.8e-112;
5; Mismatches 21;
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 94.8%;
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NEDLINE-2017556; PubMed-10710308;
NEDLINE-20175766; PubMed-10710308;
Claza M., Scarlato V., Masjanani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Huddt E., Knapp B., Blair E., Mason T., Tettelin H.,
Mocod D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.,
"Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                   NTNA----SSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGD
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
001-DEC-2001 (GRABILE ROPELN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
                                                                                          Indels
EMBL; AF226359; AAF42508.1; -.
SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;
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94.8%; Score 2861; DB 2;
Best Local Similarity 94.8%; Pred. No. 4.6e-112;
Matches 567; Conservative 5; Mismatches 22;
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SEQUENCE FROM N.A.
STRAIN=NGH15;
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e encoding a novel outer
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Proteobacteria; beta subdivision; Neisseriaceae;
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                                                                                Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennin "Identification and characterization of a gene encoding membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF1205181; AAF42530.1;
EMBL, AF120507; AAK68868.1;
                                                                                                                                                                                       62763 MW; E6C7AEF0BBBA63CB CRC64;
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Last sequence update)
Last annotation update)
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94.6%; Pred. No. 8.2e-112;
Live 6; Mismatches 22;
 Whole-Genome Sequencing.";
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
NHHA OUTER MEMBRANE PROTEIN.
                Science 287:1816-1820(2000)
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MEDLINE-20175756; PubMed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
NCBI_TaxID=487;
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennin "Identification and characterization of a gene encoding membrane protein of Naisseria meningitidis."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AFIST603: AAK68864.1; -
SEQUENCE 598 AA, 62687 MW; 18CEFFE6410A15DF CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                    94.5%; Score 2852; DB 2;
larity 94.6%; Pred. No. 1.1e-111;
Conservative 5; Mismatches 23;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           54 DDDLYLEPVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis.
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
NCBL_TRAXID=487;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                    1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFAT-----VQASTTD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKQNTNENTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAET
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Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.; "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                      8;
                                                                                                                                                                                                                                                         92.9%; Score 2806; DB 2; Length 600; 92.7%; Pred. No. 9.1e-110; Live 14; Mismatches 22; Indels
                                                                                                                                                               EMBL; AF226371; AAF42520.1; -.
SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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                                                                                                                                                                                                                                                                                 Best Local Similarity 92.7%
Matches 557; Conservative
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Q9JPS3
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09JPR8 (1000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 15) Last annotation update)
01-DEC-2001 (TrEMBLrel. 19) Last annotation update)
00TER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                   Pizza M. Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini B., Gapecchi B.,
Galoctti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettellin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
Identification of Vaccine Candidates Against Serogroup B
Meningococus D.Whole-Genome Sequencing.";
EMBL; AF226378; AA&475277.1;
EMBL; AF226378; AA&476AC300D80C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 NVDEVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 NDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 ----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTT
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llarity 93.5%; Pred. No. 4.1e-109;
Conservative 12; Mismatches 19;
SEQUENCE FROM N.A.
STRAIN-NGE28;
MEDLINE-20175756; PubMed-10710308;
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Matches 557; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                    Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer
membrane protein of Neisserla meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1226383; AAR42532.1;
EMBL; AF127608; AAR68869.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   476 KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQ 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPVQRTAVVLSFRSDKEGTGEKEVTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Companducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galectti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Moxon E.R., Grandi G., Rappuoli R.; Granoff D.M., Verter C., Munch E.L., Grandi G., Rappuoli R.; Granoff D.M., Venter C., Mentification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58869.1; -. 62844 MW; BBA16EBF53C1970C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.5%; Score 2762.5; DB 2
91.7%; Pred. No. 5.9e-108;
iive 13; Mismatches 32;
                                                                 STRAIN=NGH38;
MEDLINE=20175756; PubMed=10710308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.73
Matches 549; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              599 AA;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-H38;
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61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDMAVYFNEKGVLTAREITLKAGDNLKIKQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIKQ 116
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                                                                                                                                                                                                                   Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                           Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.K., Grandi G., Rappuoli R.;
Moxon E.K., Grandi G., Rappuoli R.;
Meningococus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA
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                 Q9JES7;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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92.3%; Pred. No. 8.5e
iive 14; Mismatches
591
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20175756; PubMed=10710308;
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                                                                                                                                                                                       Neisseria meningitidis
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Matches 552; Conserv
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                                                                                                                                                                                                                                          NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                STRAIN=BZ147
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STRAIR=MCSB / SERGGROUP B;
STRAIR=MCSB / SERGGROUP B;
MEDIATR=MCSB / SERGGROUP B;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodoson R.J.,
Melson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Dalle E., Cittone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khourl H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SPECIES. Menchightidis; STRAIN-PMC21;
SPECIES. Menchightidis; STRAIN-PMC21;
SPECIES. Menchightidis; STRAIN-PMC21;
"Identification and characterization of a gene encoding a novel outer membrane protein of Nelsseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226375; AAF42524.1;
EMBL; AF226375; AAF42516.1;
EMBL; AF226370; AAF42519.1;
EMBL; AF226370; AAF42519.1;
EMBL; AF226370; AAF42519.1;
EMBL; AF2563710; AAF42519.1;
EMBL; AF2563710; AAF42519.1;
EMBL; AF263710; AAF42519.1;
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Meisseria meningitidis, and
Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                                                                                                                                                                                                                                                                                                                                              DECORDED FROM N.A.

STRAIN=MCSB (SEROGROUP B, BZ169, BZ83, AND H44/76;

WEDLINES-20179756; PubMed=10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

Calectri C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffiles A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.4%; Score 2758.5; DB 16; Length 591; 92.3%; Pred. No. 8.5e-108; Live 14; Mismatches 21; Indels 11;
                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLRel. 19, Last annotation update)
01-DEC-2001 (TREMBLREL GNA992 (ADHESIN) (NHA OUTER MEMBRANE
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                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 287:1809-1815(2000).
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Best Local Similarity 92.3$
Matches 552; Conservative
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                     NCBI_TaxID-487, 491;
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SEQUENCE FROM N.A.
                                             Q9JR18
                                                                  Q9JR18
RESULT 13
Q9JR18
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NTNENTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGD 176
                   -----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD 174
                                                                236
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                                                                                                                                                                                                                                                                    GTTATVSKDDQGNITVWIDVNVGDALNVNOLONSGWNLDSKAVAGSSGKVISGNVSPSKG 416
                                                                                                                                                                                                                                                                                                                                       417 KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK 476
                                                                                                                                                                                                                                                                                                                                                         415 KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSK 473
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                                                                                                                                                                                                                                                                                                                                                                                                                          57 LYLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNWGVYFDKKGVLTAGTITLKAGDNLKIK 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 Q-----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MC58;
Peak I.R., Sirkhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
Patalise and obsaccterisation of a gene encoding a novel out
membrane protein of Neisseria meningitidis.";
Submitted (FBE-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125375; AAK09243.1;
EMBL; AF125375; AAK09243.1;
SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;
                                                                TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                    175 TIVHLINGIGSTLIDTLLINTGATINVINDINVIDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                   SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDK
                                                                                                                                                       GENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK
                                                                                                                                                                                                                       295 GENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKEETVTSGTNVTFASGK
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92.0%; Pred. No. 1.7e-107;
tive 13; Mismatches 23;
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Matches 551;
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            KGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings
Tdentification and characterization of a gene encoding a ramembrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR157606; AK68867.1;
SEMEL; AR157606; AR6887.1;
SEMEL; AR157606; AR6887.1;
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Db 235 SDNVDFVRTYDTVEFLSADTRTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDK 294

Qy 297 GENDSSTDKGEGLVTAKEVIDAVNKAGMRMKTTTANGGTGQADKFETVTSGTNVTFASGK 356

Db 295 GENGSSTDEGEGLVTAKEVIDAVNKAGMRMKTTTANGGTGQADKFETVTSGTNVTFASGK 354

Qy 357 GTTATVSKDDGONITVMYDVNVGDALNVNQLQNSGMNLDSKAVGCSGKVISGNVSPSKG 416

Db 355 GTTATVSKDDGONITVMYDVNVGDALNVNQLQNSGMNLDSKAVAGCSGKVISGNVSPSKG 416

A17 KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSK 476

A17 KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSK 476

A17 KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSK 478

Qy 477 DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNINNHIDNVDGNARAGIAQAIATAGLVQA 536

Qy 537 KLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNMINKGTASGNSRGHFGASASVGYQW 594

Db 534 KLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYQW 591
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Search completed: September 5, 2002, 10:30:29 Job time: 431 sec

12 161 13 161 14 161 15 138		18 20 21	нннн	25 27 28 28 99 84						### 40   19   42   43   19   44   19   44   17   44   17   45   16   46   16   46   16   49   15   49   49   49   49   49   49   49   4
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	protein search, using sw model	September 5, 2002, 10:24:43 ; Search time 58.77 Seconds (without alignments) 1122.645 Million cell updates/sec	US-09-700-293-2 594 1 MNKIYRIIMNSALNAWVAVSTASGNSRGHFGASASVGYQW 594	OLIGO Gapop 60.0 , Gapext 60.0	747574 segs, 111073796 residues	15	f hits satisfying chosen parameters: 49	seq length: 0 seq length: 2000000000	Post-processing: Listing first 1000 summaries	A_Geneseq_032802:*    SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*   SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*   SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*   SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*   SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*   SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*   SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*   SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*   SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*   SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
	OM protein - pi	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Word size :	Total number of	Minimum DB seq Maximum DB seq	Post-processing	Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		A surface protein	BASB029 amino acid	N. meningitidis EG	N. meningitidis PM	N. meningitidis PM	N. meningitidis PM	N. meningitidis PM	Amino acid sequenc	A surface protein	A surface protein	BASB029 amino acid
SUMMARIES	£		AAY23740	AAY57044	AAU06174	AAU06184	AAU06185	AAU06186	AAU06182	AAY27202	AAY23741	AAY23746	AAY57045
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BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.
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                                                                                                                                                               13-MAY-1998;
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                                                                                                                                                                                                                                              1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60
                                                       The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 KDs. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymersse, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis infection also be used to prevent or treat N. meningitidis infection in humans. The York N. meningitidis infection in humans in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
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        Neisseria meningitidis surface proteins useful for treating
                                     Claim 1; Page 100-101; 132pp; English.
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This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup bs strain ATCC13090. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Composition comprising an antibody olynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an eningiticity and for therapeutic or prophylactic purposes, polynucleotide, and for therapeutic or prophylactic purposes, polynucleotides and for therapeutic or prophylactic purposes, polynucleotides and polypeptides are also useful for treating infections particularly genetic immunisation. Antibodies against BASB029 polynucleotides and doutpeptides are also useful for treating infections particularly denetic immunisation fartherapeut is useful in the protein is useful for the stimulation of the immune system of an organism
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                                                                                                                                                      /note= "Encoded by AATC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 2; 74pp; English.
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Matches 594; Conservative
Neisseria meningitidis.
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                                                                                                                 Misc-difference 104
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25-JAN-2001; 2001WO-AU00069.
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                                                                                       PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPG
                                                                                             TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK
                                                                                                                                                                                           Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                 N. meningitidis EG327 surface antigen NhhA polypeptide sequence
                                                                                                            541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                                                                                 /label = C2
/note= "Conserved region 2"
                                                                                                                                                                                                                                                                                                                                                         /label= C5
/note= "Conserved region 5"
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                                                                                                                                                                                                                                               'note= "Variable region 1"
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/note= "Conserved region
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                                                                                                                                                                                                                                                                       /label= V3
/note= "Variable region
                                                                                                                                                                                                      Neisseria meningitidis strain EG327
                                                                                                                                                                                                                cocation/Qualifiers
                                                                                                                                                AAU06174 standard; Protein; 594 AA
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/note= "Variable
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/label- c1
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AAMUGABS-AAMUGABG. The modified or mutant Nhhh Polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                           New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGEND
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                                                                                                                                                                                                                                                                                                                                                       Claim 9; Fig 1; 91pp; English
25-JAN-2000; 2000US-0177917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.
Matches 594; Conservative
                                                        (UYQU ) UNIV QUEENSLAND
                                                                                                           Jennings MP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention.
                                                                                                                                                           2001-488774/53.
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                                                                                                                                                                                        N-PSDB; AAS09164.
                                                                                                           Peak IRA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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481 pvritnvapgvkegdvtnvaqlkgvaqnlnnhidnvdgnaragiaqaiataglvqaylpg 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                        Surface antigen NhhA; meningococcal disease; meningitis vaccine; mutant; mutein.
                         /label= Signal_peptide
52..407
/label= Mature_NhhA_deletion_mutant_#2
/note= "Predicted mature protein, specifically
claimed in claim 12"
                                                                                                                                                                                                               N. meningitidis PMC21 NhhA deletion mutant #2.
                                                                                                                                                                                                                                                                                        Neisseria meningitidis strain PMC21.
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                Ā
                                                                                                                           AAU06184 standard; Protein; 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Fig 7; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2000; 2000US-0177917.
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                                                                                                                                                                                      24-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peak IRA, Jennings MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488774/53.
N-PSDB; AAS09174.
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                                                                                                                                                                                                                                                                                                       Synthetic
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in algamostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface antigen NhAA deletion mutant #3.
366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                      Surface antigen NhhA; meningococcal disease; meningitis vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                             /label- Signal_peptide
52..433
/label- Mature_Nhha_deletion_mutant_#3
/note= "Predicted mature protein, specifically
claimed in claim 12"
                                                            N. meningitidis PMC21 NhhA deletion mutant #3.
                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis strain PMC21.
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                         AAU06185 standard; Protein; 433 AA
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N-PSDB; AAS09175.
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                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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Length 407;

306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365

Ouery Match 27.1%; Score 161; DB 22; Length 4(
Best Local Similarity 1100.0%; Pred. No. 1.1e-149;
Matches 161; Conservative 0; Mismatches 0; Indels

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us-09-700-293-2.oligo.rag

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antigen NhhA deletion mutant #4.
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                                                                            Conservative
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                                                                 Similarity
                        502 AA;
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                                                                                                                                                                                                                                                                                                                                                                 mutant; mutein.
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                                                                          Matches 161;
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                       Sequence
                                                        Query Match
                                                                   Local
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                                                                                                                                            366
                                                                                                                                                                                                                                                     AAU06182
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                                           306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                       DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                             Surface antigen NhhA; meningococcal disease; meningitis vaccine;
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0
                                                                                                                                                                                                                                                                                                                                                                                 /label= Signal_peptide
50..502
/label= Mature_Nhha_deletion_mutant_#4
/note= "Predicted mature protein, specifically
claimed in claim 12"
  Length 433;
                     Indels
                                                                                                                                          AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
27.1%; Score 161; DB 22; I
100.0%; Pred. No. 1.1e-149;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                        N. meningitidis PMC21 NhhA deletion mutant #4.
                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis strain PMC21
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                      AAU06186 standard; Protein; 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Fig 9; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2000; 2000US-0177917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2001; 2001WO-AU00069
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jennings MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488774/53.
N-PSDB; AAS09176.
           Similarity
                                                                                                                                                                                                                                                                                                          mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200155182-A1.
                                                                                                                                                                                                                                                   24-OCT-2001
                     161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peak IRA,
                                                                                                                                                                                                                              AAU06186;
  Query Match
             Local
                                                                                                                                                                                                                                                                                                                                                                         Peptide
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            Best Loca
Matches
                                                                                     366
                                                                                                                               426
                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                              AAU06186
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh (ANDG182-ANDG186). The modified or mutant Nhh polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader
                                                                                                                            306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                                                                                                                                                                                                                  DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                    215 geglvtakevidavnkagwrmktttangqtgqadkfetvtsgtnvtfasgkgttatvskd 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                             Surface antigen NhhA; meningococcal disease; meningitis vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.51
/label= Signal_peptide
52.512
/label= Mature_NhhA_deletion_mutant_#1
/note= "Predicted mature protein, specifically
claimed in claim 12"
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   Length 502;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                               335 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 375
                                                                                                                                                                                                                                                                                                                                                                              426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
27.1%; Score 161; DB 22; I
100.0%; Pred. No. 1.3e-149;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N. meningitidis PMC21 NhhA deletion mutant #1.
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Length 591;

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591 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 AAY23741;
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                     Query Match
                                                                                     Matches
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spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface antigen MhAA deletion mutant #1.
                                                                                                                                                                                                                               306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                                                                                                                                                                                                                  366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis; bacterial infection; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New protein and its nucleotide sequence, useful in vaccines or diagnostic compositions for treating and/or preventing Neisseria meningitidis infections
                                                                                                                                                                 Length 512;
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                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of N. meningitidis protein ORF40-1
                                                                                                                                                                                                                                                                                                                                                             426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.1%; Score 161; DB 22; I Best Local Similarity 1100.0%; Pred. No. 1.3e-149; Matches 161; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY27202 standard; Protein; 591 AA
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98GB-0000760.
98GB-0019015.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis.
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                                                                                                                 512 AA;
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306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                                                                                                                         366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a surface protein of Neiserria menigitidis which is approximately 62 Nos. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, the form of vaccines. The proteins and antibodies can also be used to used to used to the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis surface proteins useful for treating meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                         Indels
27.1%; Score 161; DB 20; L
100.0%; Pred. No. 1.5e-149;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                           426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
                                                                                                                                                                                                                                                                                                                                                                                         424 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 104-106; 132pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY23741 standard; Protein; 591
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                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis
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                                  Local Similarity
tes 161; Conserv
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426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 GEGLUTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis surface proteins useful for treating meningitidis infections
                                                                                                                                                                                                 surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                   426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
                                                                            27.1%; Score 161; DB 20; I
100.0%; Pred. No. 1.5e-149;
ive 0; Mismatches 0;
                                                                                                                                                                                 A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 127-128; 132pp; English.
                                                                                                                              A
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                                                                                                                              AAY23746 standard; Protein; 591
                                                                                                                                                                                                                                                                              98WO-AU01031.
                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS INNOVATION LTD. (UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                             97GB-0026398
                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                        Jennings MP, Moxon ER,
                                                                                                                                                                                                          immunoreactive peptide.
                                                                                                                                                                                                                          Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-418754/35.
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                                                                                                                                                                                                  protein;
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                                                                                                                                                                                                                                           W09931132-A1
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306
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table of the statement of the discussion disc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
                                                                                                                                                                                                                                                                                                                  BASB029 amino acid sequence from N. meningitidis strain H44/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by AATC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Encoded by AAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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AAY57045 standard; Protein; 591
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                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis.
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WO200155182-A1.
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particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism receiving the protein.
                                                                                              306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                                                                        366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                            N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                            Surface antigen NhhA; meningococcal disease; meningitis vaccine.
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/note- "Predicted mature protein, specifically
/note- "Predicted mature protein, specifically
claimed in claim 12"
                                                                27.1%; Score 161; DB 21; Length 591; 100.0%; Pred. No. 1.5e-149; tive 0; Mismatches 0; Indels (
                                                                                                                                                         426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
                                                                                                                                                                  "Conserved region 1"
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/note= "Conserved region 3"
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/note= "Variable region 4"
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                          Neissería meningitidis strain PMC21.
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                              AAU06171 standard; Protein; 591 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- v2
                                                                                                                                                                                                                                             24-OCT-2001 (first entry)
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/label= V1
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                                                                      Best Local Similarity 100.
Matches 161; Conservative
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                                        591 AA;
                                                                                                                                                                                                                              AAU06171;
                                         Sequence
                                                                Query Match
                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
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27.1%: Score 161; DB 22; Length 55
Best Local Similarity 100.0%; Pred. No. 1.5e-149;
Matches 161; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig 1; 91pp; English.
25-JAN-2001; 2001WO-AU00069.
                                                                       25-JAN-2000; 2000US-0177917.
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N-PSDB; AAS09161.
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DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425 

366

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426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466  Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.

Neisseria meningitidis.

WO9931132-A1

24-JUN-1999

A surface protein of Neisseria meningitidis.

(first entry)

08-SEP-1999

AAY23737;

AAY23737 standard; Protein; 592 AA

RESULT 14

AAY23737

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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AGM06182-AAM06186). The modified or mutant Nhh polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain EG329 is 1 of 10 Nhha Polypeptide sequences the contract of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                         /not_
|109.120
|/label= C2
|^^^^= "Conserved region 2"
/label= Cl
/note= "Conserved region 1"
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/note= "Conserved region 5"
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/note= "Conserved region 3"
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/label= V3
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/note= "Variable region
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                                                              label- Vl
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N-PSDB; AAS09165.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kIt for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis surface proteins useful for treating meningitidis infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.1%; Score 161; DB 20; I
100.0%; Pred. No. 1.5e-149;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 86-87; 132pp; English.
                                                                                                                                                                                                                                                                                    Peak IRA;
                                                                                                                                                                                                                                             (ISIS-) ISIS INNOVATION LTD. (UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                            98WO-AU01031.
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                                                                                                                                                                                                                                                                                    Jennings MP, Moxon ER,
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N-PSDB; AAX85788.
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Matches 161;
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Length 591; 0; Indels

Score 161; DB 22; I Pred. No. 1.5e-149; O; Mismatches 0;

27.1%; Scur 100.0%; Pre 0;

Matches 161; Conservative

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Similarity

Local

Query Match

306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365

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Search completed: September 5, 2002, 10:31:59 Job time: 436 sec
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Best Local Similarity 100.0%; Pred. No. 5.9e-127;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps
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52..513
/label= Mature_NhhA_deletion_mutant
/note= "predicted mature protein, specifically
claimed in claim 12"
                        425 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 465
                                                                                                                                                                                                                                                                                                           N. meningitidis H41 NhhA deletion mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                               AAU06183 standard; Protein; 513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis strain H41.
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N-PSDB; AAS09173.
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; Search time 25.6 Seconds (without alignments) 566.750 Million cell updates/sec 13, Appl 5, Appli 5, Appli 13, Appl Appli Appli Appli Appli Appli Appli Appli Appli Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Sequence 9, Sequence 9, Description Sequence 1 sednence sed Sequence Sequence Sequence .....TASGNSRGHFGASASVGYQW Sequence Sequence Sequence Sequence 41 /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/Pus.coMB.pep:\*
/cgn2\_6/ptodata/2/iaa/packfilesl.pep:\* 4.5 Compugen Ltd /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\* /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\* parameters US-09-377-155-32 US-08-913-942-2 US-08-409-995-2 US-08-685-467-2 231628 segs, 24425594 residues 5, 2002, 10:28:13 summaries SUMMARIES GenCore version Copyright (c) 1993 - 2000 protein search, using sw model OLIGO Gapop 60.0 , Gapext 60.0 MNKIYRIIWNSALNAWVAVS. Total number of hits satisfying chosen Issued\_Patents\_AA:\* Post-processing: Listing first 1000 seq length: 0 seq length: 2000000000 US-09-700-293-2 DB Length September % Query Match 1 100.0 100.0 27.1 15 Score Title: Perfect score: Scoring table: .. Minimum DB Maximum DB OM protein Word size Sequence: Searched: Database Run on: Result g

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LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 240

LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV

DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDKGEND 300

TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE 420

361

SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA

301

NINASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH 180

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361 TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE 420
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APPLICANT: DEBNINGS, Michael Paul
APPLICANT: MOXON, B. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1999-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRICA PAPLICATION NUMBER: PCT/AU98/01031
PRIOR PELICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard
                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09377155 Patent No. 6197312 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09377155 Patent No. 6197312
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; ORGANISM: Neisseria meningitidis
US-09-377-155-11
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SEQ ID NO 11
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US-09-377-155-11
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US-09-669-974-9
Sequence 9, Application US/09669974
Factor No. 633373
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 06504/0128
CURRENT FILING DATE: 200-09-26
FRIOR FILING DATE: 1999-08-19
FRIOR FILING DATE: 1999-12-12
NUMBER OF SEO ID NOS: 33
SOFTWARE: PALENTING DATE: 1997-12-12
SOFTWARE: PALENTING DATE: 1997-12-12
SOFTWARE: PALENTING DATE: 1997-12-12
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                                                                                                                                    541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                                                                                                                                      Ouery Match 27.1%; Score 161; DB 4; Length 591; Best Local Similarity 100.0%; Pred. No. 33e-144; Matches 161; Conservative 0; Mismatches 0; Indels
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366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
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100.0%; Pred. No. 3.3e-144;
tive 0; Mismatches 0;
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
SOFTWARE: PATCHIN VOR: 2.0
                            GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JUNINIOS, Michael Paul
APPLICANT: JUNINIOS, Michael Paul
ITILE OF INVENTION: ROVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1909-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN ONCE: 30
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; ORGANISM: Neisseria meningitidis
US-09-669-974-21
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Best Local Similarity
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Best Local Similarity
         Patent No. 6333173
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US-09-377-155-2
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                                                                                                                                                                                                                                                                          27.1%; Score 161; DB 4; Le 100.0%; Pred. No. 3.3e-144; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PEAK, Ian Richard Anselm APPLICANT: PEAK, Ian Richard Anselm APPLICANT: DENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE PEFERNCE: 065064/0128 CURRENT APPLICATION NUMBER: US/09/69,974 CURRENT APPLICATION NUMBER: US 09/377,155 PRIOR APPLICATION NUMBER: US 09/377,155 PRIOR FILING DATE: 1999-08-19 PRIOR FILING DATE: 1999-12-14 PRIOR FILING DATE: 1999-12-12 NUMBER: GB 9726398.2 NUMBER OF SEQ ID NOS: 33 SEQ ID NO S: 33 SEQ ID NO S: SEQ ID NOS: 30 SEQ I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/09669974 Patent No. 6333173
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                                                                                                                     ) TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21
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                               PatentIn Ver. 2.0
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Best Local Similarity 100.0
Matches 161; Conservative
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Best Local Similarity 100.(
Matches 161; Conservative
NUMBER OF SEQ ID NOS:
                               SOFTWARE: Pat
SEQ ID NO 21
LENGTH: 591
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434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKE 493
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US-09.377-155-17
Sequence 17, Application US/09377155
Patent No. 6197312:
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anseln
APPLICANT: PEAK, Ian Richard Anseln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/09669974 Patent No. 6333173 GENERAL INFORMATION:
                      TYPE: PRT (CRGANISM: Neisseria meningitidis US-09-377-155-19)
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US-09-669-974-19
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US-09-669-974-19
LENGTH: 589
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                      366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                             365 DQGNITVWYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 424
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105-09-377-155-19
Sequence 19, Application US/09377155
Patent No. 6197312
GRNERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: DENNINGS, Michael Paul
TITLE OF INVEWTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 06504/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR PLILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PEAK, IGAN RICHARD ABSELM
APPLICANT: PEAK, IGAN
APPLICANT: DENNIGOS, MICHAEL PAUL
APPLICANT: MOXON E. RiCHARD
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 05064/0128
CURRENT PELICATION NUMBER: US/09/669, 974
CURRENT PELING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377, 155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-11-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1999-12-14
SPIOR APPLICATION UNBER: GB 9726398.2
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALENTH: 592
LENGTH: 592
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US-09-669-974-2
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US-09-669-974-2
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432 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKE 491
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                                                                                                                                              US-09-377-155-5; Sequence 5, Application US/09377155; Patent No. 6197312
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; ORGANISM: Neisseria meningitidis
US-09-377-155-5
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                                494 GDVTNVAQLKGVAQNLNN 511
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4atches 138; Conservative
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LENGTH: 598
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Best Local Similarity 100.0%; Pred. No. 2e-122;
Matches 138; Conservative 0; Mismatches 0;
           APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: OFTANU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
PRIOR FILING DATE: 1997-12-12
RIOR FILING DATE: 1997-12-12
SOFTWARE: PALENTIN VET: 2.0
SEQ ID NO 17
LENGTH: 592
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100.0%; Pred. No. 2e-
live 0; Mismatches
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: BENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
ITILE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 06504/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PS/AU98/01031
PRIOR PILING DATE: 1999-08-19
PRIOR PILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
SPRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ; ORGANISM: Neisseria meningitidis US-09-669-974-17
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Best Local Similarity 100.0
Matches 138; Conservative
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100.0%; Pred. No. 2e-122;
+ive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Paul
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
ITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN OS: 33
APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: JONONON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: 19509-08-19
PRIOR APPLICATION NUMBER: PCT/AU08/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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Query Match 23.2%; Score 138; DB 4; Length 598; Best Local Similarity 100.0%; Pred. No. 2e-122; Matches 138; Conservative 0; Mismatches 0; Indels
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CURRENT FILING BATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR PILING DATE: 1999-08-19
PRIOR PILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFFWARE: PATCHIN VET. 2.0
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; ORGANISM: Neisseria meningitidis
US-09-669-974-5
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Ryfettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Accession: G81133
A;Accession: G81133
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-591 <TET>
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A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0992
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1685.678 Million cell updates/sec
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                                                                                                                                     5, 2002, 10:29:43; Search time 33.86 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd
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probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A8188
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre atture 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
A; Reference number: A81775; MUID: 20222556
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-592 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737 A;Experimental source: serogroup A, strain 22491 C;Genetics:
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100.0%; Pred. No. 5e-121;
ive 0; Mismatches 0; Indels
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27.1%; Score 161; DB 2; Le
100.0%; Pred. No. 8.7e-156;
iive 0; Mismatches 0;
Query Match 27.1 Best Local Similarity 100. Matches 161; Conservative
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 5, 2002, 10:32:38; Search time 19.19 Seconds (without alignments) 1198.510 Million cell updates/sec Run on:

US-09-700-293-2 594 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASASVGYQW 594

Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters: 15 Word size :

0

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt\_40:\* Database :

SUMMARIES

Description % Query Score Match Length DB 7 . 9 Result

No matches found

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Search completed: September 5, 2002, 10:39:36 Job time: 418 sec

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STRAIN-EG327;
STRAIN-EG327;
STRAIN-EG327;
STRAIN-EG327;
STRAIN-EG327;
STRAIN-EG327;
SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3A8EA2 CRC64;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=487.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 594; Conservative 0; Mismatches
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             Q93QY5
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099ps9 m
099ps8 m
099ps8 m
093ps7 m
093ps1 m
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09jps3 r
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09jpt0 r
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             GenCore version
Copyright (c) 1993 - 2000
                                                                 protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Q9JPS3
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Q9JPS7
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sp_human:*
sp_invertebrate:*
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sp_phage:*
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
NCBL_TAXID-487;
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STARL-NO3/8B, AND BZ232;

MEDLINE-2016756; Pubwed-10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Pizza M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

Galecti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

Ratti G., Santini L., Savino S., Scarselli M., Storni B., Zuo P.,

Ratti G., Santini L., Savino B., Balair E., Mason T., Tettelin H.,

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Science 287:1816-1820(2000)

"Embl. AFP226375; ARP42251:]

EMBL; AFP26375; ARP42251:]

SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04846 CRC64;
                                                                                                                                               13 Q9JP13 PRELIMINAL...
Q9JP13;
Q9JP13;
Q10CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 16, Last annotation update)
01-MRR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
GNA992.
Nelsseria meningitidis.
Nelsseria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
481 PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPG 540
                                             374 YDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT 433
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0UTER MEMBRANE PROTEIN GNA992.
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374 YDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT 433
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MEDIANS-20175765, PubMed=10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Pizza M., Scarlato V., Masignani V., Gapecchi B.,

Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Ratti G., Santini L., Savino B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

Moningococus by Whole-Genome Sequencing.";

Science 287:1816-1820(2000).

Science 287:1816-1820(2000).

SEQUENCE 594 AA; 62114 MW; IE2A63A78F53D256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-228, AND 1000;

MEDLINE-20175756; PubMed-10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jendings G.T., Baldi L., Bartolini E., Capecchi B.,

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Ratti G., Santini L., Savino B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

Moningococus D.W., Vaccine Candidates Against Serogroup B

Meningococus D.W., Sequencing ",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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EMBL, AP226356; AAF42505.1; -.
SEQUENCE 595 AA, 62120 MW; 8212C96380142BFC CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
GNA992.
BACSERIA meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                      434 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKE 493
                                                                                            GDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRG 553
                                                                                                                                     GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                          374 YDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT 433
                       Gaps
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MEDLINE-20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Pizza M., Jeannings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
I'dentification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
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   Length 595;
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100.0%; Pred. No. 3e-147;
ive 0; Mismatches 0; Indels
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SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;
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                                                                                                                                                                    EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                                                                                                                                             37.2%; Score 221; DB 2; Lv 100.0%; Pred. No. 4e-204; ive 0; Mismatches 0;
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01-OCT-2000 (TrEMBLrel. 15, Created)
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                      221; Conservative
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Best Local Similarity
           Similarity
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                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=487;
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Matches 162;
  Query Match
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306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
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                                                                                                                                                                    Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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"Identification of Vaccine Candidates Against Serogroup B
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SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDD 467
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).
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                                                                                                                                                                                                                                                                                               STRAIN=SWZ107;
MEDLINE=20175756; PubMed=10710308;
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                                                                 OUTER MEMBRANE PROTEIN GNA992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis.
Bacteria; Proteobacteri
                                                                                                                                     Neisseria meningitidis.
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                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=487;
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Length 599;

27.3%; Score 162; DB 2;

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SEQUENCE FROM N.A.
STRAIN-MCS8 / SERGGROUP B;
MEDLINE-2017575; PubMed-10710307;
Pettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salaberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Oin H., Vamathevan J., Gill J., Scarlato V., Masgnani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., Moxon E.R., Rappuoli R., Venter J.C., MCS8."
                                                                                                                                                                                  Peak I.R., Stikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis:',
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ARISF606; AAK68867.1; -.
SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
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SEQUENCE FROM N.A.

STAIN-WESS / SENCENCUP B, BZ169, BZ83, AND H44/76;

MEDLINE-20175756; PubMed=10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Galeotti C. M., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

Rati G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Rati G., Santini E., Rappp B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

Meningococcus by Whole-Genome Sequencing.";
        Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis, and selesseria meningitidis (serogroup B).
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria NCBL_TAXID=487, 491;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLRel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.1%; Score 161; DB 2; Length 591; 100.0%; Pred. No. 2.7e-146; tive 0; Mismatches 0; Indels
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                                                                                                                         SEQUENCE FROM N.A.
                                               NCBI_TaxID-487
                                                                                                                                                        STRAIN=EG329
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                                                                                                                                                            366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                            306 GEGLUTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
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27.1%; Score 161; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.76-146;
Matches 161; Conservative 0; Mismatches 0; Indels
100.0%; Pred. No. 3e-147;
Live 0; Mismatches 0; Indels
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01-DEC-2001 (TTEMBLrel. 19, Created)
01-DEC-2001 (TTEMBLrel. 19, Last sequence update)
01-DEC-2001 (TTEMBLrel. 19, Last annotation update)
NHHA OUTER MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDD 472
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BZ147;
MEDLINE-20175756; Pubmed-10710308;
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                                       Conservative
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    Best Local Similarity
Matches 162; Conserv
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RA SPECIES—N. meningitidis; STRAIN—PMC21;
RA PERK I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AR226375; AAR42524.1; -..
DR EMBL; AR226377; AAR42516.1; -..
DR EMBL; AR226370; AAR42516.1; -..
DR EMBL; AR226371; AAR68872.1; -..
DR EMBL; AR157611; AAR68872.1; -..
DR EMBL; AT157611; AAR68872.1; -..
DR TIGR; NMB0992; -..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-MC58;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
"Identification and characterisation of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF125375; AAK09243.1;
SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;
                                                                                                                                                                                                                                                                                            DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQGNITVMYDVNVGDALNVNOLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                                                                                                                                                                                                    27.1%; Score 161; DB 16; Length 591; 100.0%; Pred. No. 2.7e-146; ive 0; Mismatches 0; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER MEMBRANE PROTEIN.
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Best Local Similarity 100.0%; Pred. No. 2.7e-146;
Matches 161; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 161; Conservative
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Q9AQF0
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STRAIN=P20;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Indentification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF157610; AAK68971.1;
SEQUENCE 589 AA; 61448 MW; 1F1A80CD610CB230 CRC64;
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                                                                                                                                                                                                                     Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisserlaceae; Neisseria.
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EMBL, AF226384; AAF42533.1; -

EMBL, AF226362; AAF42511.1; -

EMBL, AF226362, AAF42512.1; -

SEQUENCE 589 AA, 61520 MW; 2B2A95D4868566A6 CRC64;
                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0UTER MEBREANE PROTEIN GNA992.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NHHA OUTER MEMBRANE PROTEIN.
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   589
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STRAIN-NGP165, 90/18311, AND 93/4286;
MEDLINE-20175756; Pubmed-10710308;
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SEQUENCE FROM N.A.
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Search completed: September 5, 2002, 10:39:11
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Identification of Vaccine Candidates Against Serogroup B Meningococus by Whole-Genome Sequencing.";
Identification of Savino Sequencing.";
EMBL; AF226378; AAR42571:;
EMBL; AF226378; AAR42571:;
EMBL; AF226378; AAR425771:
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                     23.2%; Score 13%; DB 2; Length 589; 100.0%; Pred. No. 4e-124; Live 0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NHHA OUTER MEMBRANE PROTEIN.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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SEQUENCE PROM N.A.
STRAIN-NGE28;
MEDLINE-20175756; Pubmed-10710308;
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Matches 138; Conservative
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STRAIN-H41;
STRAIN-H41;
STRAIN-H41;
Jeak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Meak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
membrane protein and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
EMBL, SUBMITER G. J., J., STREME, S
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Best Local Similarity 100.6
Matches 138; Conservative
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1116.975 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Surface protein; surface glycoprotein; infection; vaccine;
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           immunoreactive peptide.
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                                  Neisseria meningitidis
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N-PSDB; AAX85798.
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                                                                              The invention provides proteins (AAY27201-245) from Neisseria meningitidis (strains A and B) and nucleic acid sequences (AAX9123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition or a diagnostic composition. The composition is also bacteria, especially Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                      EGIGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKONGTNFTYSLKKDLTDLTS 138
                                                                                                                                                                                                                                                                                                                                   VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTN 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVN 318
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                                                                                                                                                                                                                                                                      19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK 78
                                                                                                                                                                                                                                                                                   New protein and its nucleotide sequence, useful in vaccines or diagnostic compositions for treating and/or preventing Neisseria meningitidis infections
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                                                                                                                                                                                                                      Score 573; DB 20; Length 591;
                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                               A surface protein of Neisseria meningitidis.
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                                                         Claim 1; Page 62; 123pp; English.
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Matches 573; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a surface protein of Neiserria menigitidis which is approximately 62 kms. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, the form of vaccines. The proteins and antibodies can also be used to such the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis surface proteins useful for treating meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 127-128; 132pp; English.
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98WO-AU01031.
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                                                                                                                (ISIS-) ISIS INNOVATION LTD.
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Best Local Similarity 100.(
Matches 573; Conservative
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meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain PWC21 is 1 of 10 NhhA polypeptide sequences (AAU06111-AAU06180) from 10 different N. meningitidis strains given in the present invention.
                     New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                 The present invention relates to the isolation of novel Neisseria
                                                             Claim 9; Fig 1; 91pp; English
  N-PSDB; AAS09161
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                  N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
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claimed in claim 12"
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                                                                                                                                                           EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS 138
                                                                      Gaps
                                                                                                 78
                                                                                                                VNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVN
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                                                                                                                                                                                                                     VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTN
                                                                                                                                                                                                                                                                             VINDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTT
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                                         Length 591;
                                                                    0; Indels
                                       97.0%; Score 573; DB 22;
100.0%; Pred. No. 0;
ive 0; Mismatches 0;
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                                                     Similarity 100.
591 AA;
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367 nitvmydvnvgdalnvnglgnsgwnldskavagssgkvisgnvspskgkmdetvninagn 426
                                                 427 NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAP 486
                                                                              487 GVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGG 546
                                                                                                                                                                              N. meningitidis EG329 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                                                                                                               547 TYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
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/label= C1
/note= "Conserved region 1"
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/note= "Conserved region 3"
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"Conserved region 2"
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237..591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis strain EG329.
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAU06175 standard; Protein; 591 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488774/53.
N-PSDB; AAS09165.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEG 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 Non. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis surface proteins useful for treating N. meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 88.8%; Score 525; DB 20; Length 591; al Similarity 100.0%; Pred. No. 0; 525; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                             Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.
                                                                                                                                                 A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 104-106; 132pp; English.
AAY23741 standard; Protein; 591 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peak IRA;
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                                                                                             08-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jennings MP, Moxon ER,
                                                                                                                                                                                                                                                                               Neisseria meningitidis.
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N-PSDB; AAX85793.
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N. meningitidis PMC21 NhhA deletion mutant #1.
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                                                                                                                                   meningtidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningtidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningtidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningtidis strain S6329 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningtidis strains given in
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  New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                      present invention relates to the isolation of novel Neisseria
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100.0%; Pred. No. v.
... 0; Mismatches
New NhhA surface antigen polypeptides
Neisseria meningitidis, useful in prod
                                                                               Claim 9; Fig 1; 91pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
nes 525; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                        591 AA;
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA ANDOGESA-ANUGISEO. The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface antigen NhAA deletion mutant #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 TDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNT 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NhhA; meningococcal disease; meningitis vaccine;
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0
                                                                                                                                             Location/Qualifiers
1..51
52..512
Alabol = Mature_NhhA_deletion_mutant_#1
/note= "predicted mature protein, specifically
claimed in claim 12"
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                                                                    Neisseria meningitidis strain PMC21 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Fig 5; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2000; 2000US-0177917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488774/53.
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Surface antigen
                       mutein.
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                          mutant;
                                                                                                                                                                       Peptide
                                                                                                                                                                                                                           Protein
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119 KQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVH 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutant; mutein
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VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN 433
           434 GKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDV 493
                                                      494 TNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAG 553
                                                                                                59 DLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a surface protein of Neiserria menigitidis which is approximately 62 Nea. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans. The N. meningitidis is infection in humans. The N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20; Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis surface proteins useful for treating meningitidis infections
                                                                                                                                                                                                                                                                                               Surface protein; surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                             475 yaigyssisdggnwiikgtasgnsrghfgasasvgygw 512
                                                                                                                               554 YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                          A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.1%; Score 432; DB illarity 99.8%; Pred. No. 0; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 86-87; 132pp; English.
                                                                                                                                                                                                          AAY23737 standard; Protein; 592 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peak IRA;
                                                                                                                                                                                                                                                                                                                                                                                                                   97GB-0026398.
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                                                                                                                                                                                                                                                     08-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jennings MP, Moxon ER,
                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                         immunoreactive peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-418754/35.
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Matches 532; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            592 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   12-DEC-1997;
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                                                                                                                                                                                                                                 AAY23737;
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SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA 358
                                                                                                                                                                                                                                                                                                                                                                           419 TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKP 478
                                                                                                                                                        TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 VRITINVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGK
                                                     LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Surface antigen NhhA; meningococcal disease; meningitis vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1...51
/label= Signal_peptide
52..4abel= Mature_NhhA_deletion_mutant_#3
/note= "Predicted mature protein, specifically
claimed in claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    539 SMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N. meningitidis PMC21 NhhA deletion mutant #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis strain PMC21
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU06185 standard; Protein; 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2001; 2001WO-AU00069.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488774/53.
N-PSDB; AAS09175.
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Misc-difference 92

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                                                                                       The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AMMOGANGES-AANGGI86). The modified or mutant Nhh polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface antigen NhhA deletion mutant #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
Infection; treatment; prevent; antibacterial drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 SLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRI 510
                                                                                                                                                                                                                                                                                                                                                                                                                         211 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                        NLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSV 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIK 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGW 390
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
 New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASB029 amino acid sequence from N. meningitidis strain H44/76.
                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                           Length 433;
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                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                        64.5%; Score 381; DB 100.0%; Pred. No. 0; ive 0; Mismatches
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New NhhA surface antigen polypeptides
Neisseria meningitidis, useful in prod
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Misc-difference 90
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                                                               Claim 12; Fig 8; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                        Query Match 64.5
Best Local Similarity 100.
Matches 381; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                         433 AA
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                                                                                                                                                                                                                                                                                                          Sequence
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This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain H44/76. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSP) protein. The invention relates to BASB029 polynucleotide sequences (AAX57044-Y57045) and their immunogenic fragments. PASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 particularly bacterial infections. The protein is useful in the combinant scenening and development of antibacterial drugs. Pused recombinant protein is useful in the immune system of an organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 NFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDE 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 591;
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Pred. No. 0;
                                                                                                                                 AAA"
                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
              note= "Encoded by
                                                         /note= "Encoded by Misc-difference 123
                                                                                                                                 ρλ
                                                                                                                                                             /note= "Encoded by
                                          /note= "Encoded
                                                                                                                               /note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 2; 74pp; English.
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99.8%;
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Matches 467; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receiving the protein.
                                                                                                                                             389
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-053103/04.
                                                        Misc-difference 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             591 AA;
                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ39865
                                                                                                                Misc-difference
                          Misc-difference
                                                                                                                                             Misc-difference
                                                                                                                                                                                         W09958683-A2
                                                                                                                                                                                                                                                    07-MAY-1999;
                                                                                                                                                                                                                                                                                13-MAY-1998;
                                                                                                                                                                                                                      18-NOV-1999
                                                                                                                                                                                                                                                                                                                                             Ruelle J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface antigen NhAA deletion mutant #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peak IRA, Jennings MP;
                                                                   407 AA;
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                                                                                                       Query Match
Best Local Sim
Matches 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU06186;
                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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             The present invention relates to the isolation of novel Neisseria meniagitidals mutant polypeptides of the surface antigen Nhh. Manneniagitidals mutant polypeptides of mutant Nhh polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of
304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 363
                                            DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423
                                                                                         424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITN 483
                                                                                                                                      484 VAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPCKSMMAI 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                              Surface antigen NhhA; meningococcal disease; meningitis vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- Signal_peptide
52..407
/label- Mature_NhhA_deletion_mutant_#2
/note- "Predicted mature protein, specifically
claimed in claim 12"
                                                                                                                                                                                    544 GGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                N. meningitidis PMC21 NhhA deletion mutant #2.
                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis strain PMC21.
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                                                                                                                                                                                                                                                                   AAU06184 standard; Protein; 407 AA
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N-PSDB; AAS09174.
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                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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237 NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGE 296
                                                                                                                       297 NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGT 356
                                                                                                                                                                                                    357 TATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKM 416
                                                                                                                                                                                                                                                                                                                                                              477 KPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLP 536
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                417 DETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             537 GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Surface antigen NhhA; meningococcal disease; meningitis vaccine;
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/label= Mature_NhhA_deletion_mutant_#4
/note= "Predicted mature protein, specifically
claimed in claim 12"
DB 22; Length 407;
0;
                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N. meningitidis PMC21 NhhA deletion mutant #4.
                  60.1%; Score 355; DB
100.0%; Pred. No. 0;
live 0; Mismatches
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Synthetic.
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                                                         Conservative
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                                       Similarity
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08-SEP-1999
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          14-JAN-1999;
                             09-OCT-1998;
                                                  01-SEP-1998;
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                                        14-JAN-1998
                                                                                                                                                                                                                                                                                                                                     Best Local Sim
Matches 175;
                                                                                          Grandi G,
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                                                                                                                                                                                                                                                                                               Sequence
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                                                                                               The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhA (AANOS182-AANOS186). The modified or mutant NhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface antigen NhhA deletion mutant #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                          DETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLP 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGE 296
                                                                                                                                                                                                                                                                                                                           NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGT 356
                                                                                                                                                                                                                                                                                                                                                                     TATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKM 416
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                     New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
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                                                                                                                                                                                                                                                                         DB 22; Length 502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of N. meningitidis protein ORF40
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                                                                                                                                                                                                                                                                    60.1%; Score J.J.,
100.0%; Pred. No. 0;
+ive 0; Mismatches
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                                                                               Claim 12; Fig 9; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 355; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis
        WPI; 2001-488774/53.
N-PSDB; AAS09176.
                                                                                                                                                                                                                                         502 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 INGDITVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 KAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                         diagnostic compositions for treating and/or preventing Neisseria meningitidis infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKD 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 245;
                                                                                                                                                                              Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Surface protein; surface glycoprotein; infection; vaccine;
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Pred. No. 7.7e-169;
0; Mismatches 0;
                                                                                                                                                                            Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface protein of Neisseria meningitidis
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100.0%; Pre
                                                                                                                                                                              Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 61; 123pp; English.
                                         98GB-0022143.
98GB-0000760.
98GB-0019015.
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99WO-IB00103
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                                                                                                                                                                                 Masignani
                                                                                                                                                                                                                        WPI; 1999-444400/37.
                                                                                                                                  (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 AA;
                                                                                                                                                                                                                                               N-PSDB; AAX99123
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us-09-700-293-4.oligo.rag

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This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain ATCC13090. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (RFF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and polypeptide sequences (AAZ30864-X39864-Z39865) and polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a memmal-. Compositions containing a RASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a memmal-. Composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the Stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the protein is useful in the protein is useful in the immune system of an organism protein as useful in the immune system of an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 GEGLUTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.2%; Score 161; DB 21; I Best Local Similarity 100.0%; Pred. No. 2.9e-154; Matches 161; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= C2
/note= "Conserved region 2"
117..126
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/note= "Conserved region 1"
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/note= "Variable region
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                                                                                                                               Claim 4; Fig 2; 74pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                      meningitidis which is approximately 62 kbs. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis infection in humans. The N. meningitidis infection in humans, prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
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                                                                                                                                                                                                                                                                                    The present sequence represents a surface protein of Neiserria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 594;
                                                                                                                                                 Neisseria meningitidis surface proteins useful for treating meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.2%; Score 161; DB 20; Length 59
100.0%; Pred. No. 2.9e-154;
ive 0; Mismatches 0; Indels
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Misc-difference 104
/note= "Encoded by AATC"
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                                                                                                                                                                                                                             Claim 1; Page 100-101; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY57044 standard; Protein; 594 AA.
                     Jennings MP, Moxon ER, Peak IRA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-EP03255
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Best Local Similarity 100.
Matches 161; Conservative
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                                                                  1999-418754/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             594 AA;
                                                                                              N-PSDB; AAX85792
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Gaps

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Length 594; 0; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
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100.0%; Pred. No. 2.9e-154;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                            /label= C4
/note= "Conserved region 4"
                    /note-
127.190
/label C3
` -+a= "Conserved region 3"
/label= V2
/note= "Variable region 2"
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/note= "Variable region 4"
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/note= "Variable region 3"
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                                                                                                                                                                                                                                                                                                       25-JAN-2001; 2001WO-AU00069
                                                                                                                                                                                                                                                                                                                                    25-JAN-2000; 2000US-0177917.
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Best Local Similarity 100.
Matches 161; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            he present invention.
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N-PSDB; AAS09164.
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Search completed: September 5, 2002, 10:32:01 Job time: 438 sec

32, Appl 4, Appli 4, Appli 33, Appli 4, Appli 33, Appl 36, Appl 47, Appl 6, Appli 6, Appli 6, Appli

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ALNVNOLONSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNID 438
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US-09-669-974-32

US-08-268-347-44

US-08-685-467-4

US-08-685-467-4

US-08-913-942-4

US-09-669-974-33

US-09-268-347-35

US-09-268-347-35

US-09-268-347-36

US-09-268-347-36

US-08-995-6

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100.0%; Pred. No. v,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: JONONN, E. Richard APPLICANT: MONON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: 6B 9726398.2
PRIOR FILING DATE: 1999-12-12
RIGHTOR FILING DATE: 1999-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-377_155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
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   SEQ ID NO 21
LENGTH: 591
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: DESCRIPTION IN STREET OF SUFFACE ANTIGEN
FILE REFERENCE: 055064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1999-11-14
PRIOR PLING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN OF SEQ ID NOS: 33
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Patent No. 6197312
GENERAL INFORMATION:
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379 ALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNID 438
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APPLICANT: PEAK, IAN RICHARD ANSELM
APPLICANT: MOXON. B. RICHARD
TITLE OF INVENTION: NOVEL. SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669, 974
CURRENT APLICATION NUMBER: US/09/669, 974
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1991-12-14
PRIOR FILING DATE: 1991-12-14
PRIOR FILING DATE: 1991-12-14
SOFTWARE: PALENTING NUMBER: GB 9726398.2
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NO 21.
LENGTH: 591
                                                                                                                                                                                                                        559 SSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                   559 SSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/09669974 Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          SULT 2
-09-669-974-21
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SEQ ID NO 2
LENGTH: 592
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487 GVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGG 546
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                                         88.8%; Score 525; DB
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                    GENEKAL INFUGATIONAL LINGUARTH LINGUARTH LINGUARTH LINGUARTH PEAK, IAN RICHARD PAUL APPLICANT: DENNINGS, MICHAEL PAUL APPLICANT: MOXON, E. Richard FILLE REPERENCE: 065064/0128 CURRENT PILLE NOVEL SUFFACE ANTIGEN FILE REPERENCE: 065064/0128 CURRENT PILLING DATE: 2000-09-26 CURRENT FILING DATE: 1999-08-19 PRIOR FILING DATE: 1999-08-19 PRIOR PILICATION NUMBER: US 09/377,155 PRIOR FILING DATE: 1998-12-14 PRIOR FILING DATE: 1998-12-14 PRIOR FILING DATE: 1998-12-12 SOFTWARE: PAUDR FILING DATE: 1997-12-12 SOFTWARE: PAUDR FILING
                                                                                                                                                                                               Sequence 11, Application US/09669974 Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11
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Best Local Similarity 100.
Matches 525; Conservative
                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                          US-09-669-974-11
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                                 GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard
APPLICANT: JENNINGS, Michard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 06504/0128
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1999-12-12
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Pred. No. 0;
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US-09-669-974-2
; Sequence 2, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
Sequence 2, Application US/09377155
Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Neisseria meningitidis US-09-377-155-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.1%;
99.8%;
                                                                                                                                                                                                                                                                                                     PatentIn Ver. 2.0
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Best Local Similarity 99.8%
Matches 532; Conservative
                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 33
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304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 363
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SUBFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR PLICATION NUMBER: PET/AU98/01031
PRIOR PLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR PLICATION NUMBER: GB 9726398.2
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 2.0
  CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
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US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6333173
                                                                                                                                                                                                                                                       ; ORGANISM: Neisseria meningitidis US-09-377-155-9
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; ORGANISM: Neisseria meningitidis
US-09-669-974-9
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                                                                                                                                                                                      SEQ ID NO 9
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1200-09-26
PRIOR PPLICATION NUMBER: US/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFWARE: PATENTIN VEY: 2.0
LENGTH: 592
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
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                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2
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; ORGANISM: Neisseria meningitidis US-09-669-974-13
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SOFTWARE: PatentIn Ver. 2.0
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US-09-377-155-13
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LENGTH: 598
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LENGTH: 598
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426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
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                                                                                                                       GENERAL INC. 01.112.

GENERAL INCORMATION:

APPLICANT: PEAK, Ian Richard Anselm .

APPLICANT: PEAK, Ian Richard Anselm .

APPLICANT: DENNINGS, Michael Paul

APPLICANT: MOXON, E. Richard

TITLE OF INVENTION: NOVEL SURPACE ANTIGEN

FILE REFERENCE: 065064/0128

CURRENT APPLICATION NUMBER: 1999-08-19

PRIOR APPLICATION NUMBER: PCT/AU98/01031

PRIOR RILING DATE: 1998-12-14

PRIOR RILING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PALENTIN VET. 2.0

SEQ ID NO 7

LENGTH: 594
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APPLICANT: PEAK, IAN Richard Anselm
APPLICANT: DEAK, IAN Richard Anselm
APPLICANT: JUNNINGS, Michael Paul
APPLICANT: JUNNINGS, Michael Paul
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1099-08-19
PRIOR PILING DATE: 1999-08-19
PRIOR PILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1999-12-12
                                                                      US-09-377-155-7; Sequence 7, Application US/09377155; Patent No. 6197312
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.0
Matches 117; Conservative
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176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTAS 235
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236 DNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGK 292
                              238 DNVDEVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGK 294
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                                                                                                                                                                                                                                                     APPLICANT: PEAK, Ian Richard Anselm APPLICANT: PEAK, Ian Richard Anselm APPLICANT: DENNINGS, Michael Paul APPLICANT: DENNINGS, Michael Paul ITTLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 06564/0128
CURRENT APPLICATION NUMBER: U$/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER: OF SEQ. DID NOS: 33
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APPLICANT: PEAK, IAN Richard Anselm
APPLICANT: BEAK, IAN Richarl Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
ITILE OF INVENTION: NOVEL SURFACE ANTIGEN
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1099-08-19
PRIOR PILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
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; Sequence 13, Application US/09669974
; Patent No. 6333173
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ORGANISM: Neisserla meningitidis US-09-669-974-15
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US-09-377-155-17
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Matches 116;
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       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCORMATION:
APPLICANT: PERK, I BIR Richard Anselm
APPLICANT: JERMA, I BIR Richard
APPLICANT: JENAN, Michael Paul
APPLICANT: JENAN, MICHAEL PAUL
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR RILING DATE: 1999-12-12
PRIOR FILING DATE: 1999-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
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NUMBER OF SEQ ID NOS: 33
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TITLE OF INVENTION: NOVEL SUBFACE ANTIGEN FILE REFERENCE: 065064/0128

CURRENT APPLICATION NUMBER: US/09/669,974

CURRENT FILING DATE: 1909-08-19

PRIOR FILING DATE: 1999-08-19

PRIOR PLICATION NUMBER: PCT/AU98/01031

PRIOR PLICATION NUMBER: PCT/AU98/01031

PRIOR PLICATION NUMBER: GB 9726398.2

PRIOR FILING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 33

SOFTWARE PATENTING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 33

SOFTWARE PATENTING DATE: 1997-12-12
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; Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Nelsseria meningitidis US-09-377-155-15
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US-09-669-974-15
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                                                                                                           476 NKPVRITUVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYL 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 LLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEF 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 LLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEF 249
                                                        0; Gaps
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                                                                                                                                                                                                                                                  144 PGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 599
                                                                                                                                                                                                                      536 PGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
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   Length 599;
                                                        0; Indels
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19.6%; Score 116; DB 4; Le
illarity 100.0%; Pred. No. 1.5e-101;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PEAK, Ian Richard Anselm APPLICANT: PEAK, Ian Richard Paul APPLICANT: DENNINGS, Michael Paul TITLE OF INVENITON: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128 CURRENT FILLO DATE: 1999-08-19 PRIOR APPLICATION NUMBER: PCT/AU98/01031 PRIOR APPLICATION NUMBER: PCT/AU98/01031 PRIOR FILLING DATE: 1999-08-19 PRIOR FILLING DATE: 1997-12-12 NUMBER: OF SEQ ID NOS: 33

SEQ ID NO 17

SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: September 5, 2002, 10:32:33 Job time: 260 sec
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09377155 Patent No. 6197312 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-17
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VNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVN 318
                                                                                                                                                                                                                                                                                                                                                        KAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGD 378
                                                                                                                                                                                                                                                                                                                                                                                                                      ALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNID 438
                                                                                                                                                                                                    VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTN 198
                                                                                   19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK
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                                                                  VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK
                                                                                                                                    EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS
                                                                                                                                                                                                                                                                      VINDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTT
Match 97.0%; Score 573; DB Local Similarity 100.0%; Pred. No. 0; es 573; Conservative 0; Mismatches
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Query Match
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C. Species: Neisseria meningitidis
C. Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C. Accession: 681133
R. Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischman, R.D.; Dougherty, B.A. ti, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Scance, Sar, 1809-1815, 2000
A. Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; N. A. Arcession: Galli33
A. Scatus: Preliminary
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-591 <- Texts.
                                                                                               ; Search time 33.86 Seconds
(without alignments)
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probable surface f
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                                                                                                                                                                                                                                                                                  283138 seqs, 96089334 residues
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                                                                  protein search, using sw model
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C; Accession: A81888
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo; Hourby, S.J.; Churcher, C.; Klee, S.R.; Mo; Houre, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
A; Reference number: A81775; MUID: 20222556
A; Accession: A81888
A; Accession: A81888
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737
A;Experimental source: serogroup A, strain 22491
           (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis C;Species: Neisseria meningitidis C;Species: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG 353
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Matches 137; Conservative 0; Mismatches
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QQ QY Db

Search completed: September 5, 2002, 10:33:11 Job time: 208 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

Title: Perfect score: Sequence:

September 5, 2002, 10:39:36 ; search time 19.19 Seconds
(without alignments)
1192.457 Million cell updates/sec

US-09-700-293-4 591 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASASVGYQW 591

OLIGO Gapop 60.0 , Gapext 60.0

Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters: 15 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt\_40:\* Database :

Description SUMMARIES Query Score Match Length DB

Search completed: September 5, 2002, 10:39:36 Job time: 418 sec

No matches found

. 9 Result

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neisseria m haemophilus haemophilus

neisseria neisseria neisseria neisseria

09jps6 09jps5 09jqy2 09jp10 09jph0 09jph0 09jph0 09jph0

neisseria neisseria neisseria

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STRAIN-MCS8 / SERGGROUP B;
MEDLINE-20175755; PubMed=10710307;
MEDLINE-20175755; PubMed=10710307;
Eisen J.A., Ketchlum K.A., Heidelberg J., Jeffries A.C., Nelson K.E.,
Eisen J.A., Ketchlum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Felischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair E., Cittcone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIES-N. meningitidis; STRAIN-PMC21;
Peak I.R., Sirkhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis.";
                                                                                                                                                                                                                                                                                               GNA992 OR NWB0992 OR NHHA.
Neisseria meningitidis, and
Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                             PERGRONGE OF SEROGROUP B, BZ169, BZ83, AND H44/76;
MEDLINE-20175756; PubMed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon B.R., Grandi G., Rappuoli R.;
Midelification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
32 (ADHESIN) (NHHA OUTER MEMBRANE
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EMBL; AF226373, AAF4251.
EMBL; AF226373, AAF4216.1; -
EMBL; AF226377; AAF4219.1; -
EMBL; AF226374; AAF42519.1; -
EMBL; AF226374; AAF4253.1; -
EMBL; AF226374; AAF4253.1; -
                                                                                                                                                                                                                     591 AA
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                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
OUTER MEMBRANE PROTEIN GNA992 (ADHES.
          Q9JPR8
Q9JPS6
Q9JPS5
Q9JQY1
Q9JPH0
Q9JPH0
Q9JQY1
Q9JQY2
Q9JQY2
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Q9JQY2
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NCBI_TaxID=487, 491;
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                     parameters:
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Identification and characterization of a gene encoding a novel outer
membrane protein of Nelseria meningitidis.;
Submitted (JUN-1999) to the EMBL/GenBank/DBBJ databases.
EMBL; ARK6867.1; - CODC600798859C65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 YFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 ADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSK 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                  36 TAVLATLLEATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAV 95
                                                                                                                                                                                                                                                                                                                                                                                         36 TAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAV 95
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94.1%; Score 556; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 556; Conservative 0; Mismatches 0; Indels
"Identification of Vaccine Candidates Against Serogroup Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820[Ob.]. EMBL: AF26366; AF42515.1; -. SEQUENCE 591 AA; 62113 MW; 533453CAE5A9IEIF CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTN 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 VNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVN 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 KAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGD 378
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                                                                                                                                                                                                                                                                                                                                                19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK 78
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
NCBL_TARXID-407;
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                                                                                                                                                                  Query Match 97.0%; Score 573; DB 16; Length 591; Best Local Similarity 100.0%; Pred. No. 0; Matches 573; Conservative 0; Mismatches 0; Indels
                                                                     62112 MW; 7C22F3CAE7F73EC6 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCT-2011 (TrEMBLrel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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MEDLINE=20175756; PubMed=10710308;
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                                Complete proteome. SEQUENCE 591 AA;
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PRT; 591 AA.

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TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE 418
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NCBI_TaxID=487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Savino E., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
              SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
                                                                                                                                                                                                                                                                                            479 VRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQA1ATAGLVQAYLPGK
                                                                                                                                                                                                                                                                                                         LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
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                                                                                                                                                                                                                                                                                                                                                         Length 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF226377; AAF42526.1; -.
SEQUENCE 526 AA; 54732 MW; F543C4234AF807CA CRC64;
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Last sequence update)
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Mismatches 0;
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MEDLINE=20175756; PubMed=10710308;
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100.0%; Pre
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01-0CT-2000 (TIEMBLIEL 15, LA
01-MAR-2001 (TIEMBLIEL 16, LA
0UTER MEMBRANE PROTEIN GNA992.
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                                                                      YSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186
                                                                                                                      LVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQG 366
                                                                                                                                                                                                                                                                                                       NITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGN 426
                                                         RTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFT 126
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           591;
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SPAIN-MCS8;

SPAININ, SIKhanta Y., Dieckelman M., Moxon E.R., Jennin

"Identification and characterisation of a gene encoding a

membrane protein of Neisseria meningitidis.";

SUBMITTER (FEB-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF125375; AAK09243.1; -

SEQUENCE 592 AA, 62290 WW; 168986A97381EFC5 CRC64;
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01-JUN-2001 (
01-JUN-2001 (
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Best Local S:
Matches 532,
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152 KVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKR 211
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
      Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-20175756; Pubmed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Pizza M., Scarlato V., Masignani V., Giuliani E., Capecchi B.,
Comanducci M., Jennings G.T., Baldi L., Bartclini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
Rati G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Huddt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Sanders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
Identification of Vaccine Candidates Against Serogroup B
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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                                                                                                                                                                                                                                                                                                                                                                                        Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL, AR226376; AAR42525.1; -
EMBL; AF226369; AAR42518.1; -
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MEDLINE=20175756; Pubmed=10710308;
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SEQUENCE 594 AA; 62114
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MEDLINE-201756; PubMed=10710308;

MEDLINE-201756; PubMed=10710308;

MEDLINE-201756; PubMed=10710308;

A Commaducci M., Jennings G.T. Baldi L., Bartolini E., Capecchi B.,

A Galeotti C.L., Luzzl E., Manetti R., Marchetti E., More M., Nutri S.,

A Ratti G., Santhni L., Savino S., Scarselli M., Storni E., Zuo P.,

B Droker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

A Brocker M., Hundt E., Rappuoli R.;

A Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Morningococus by Whole-Genome Sequencing.";

Calence 28:1816-1820(2000).

SEQUENCE 530 AA; 55190 MW; IF836CA57598515B CRC64;
311 YDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT 370
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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Q9JPI3
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                                   KVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKR 211
                                                                      212 AASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTE 271
                                                                                                                       Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                  Gaps
                                                                                                                                                                                                                                                                                                                                                Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Companducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galecti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hudd E., Knapp B., Blair E., Mason T., Tettelin H., Moxon D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., "Identification of Vaccine Candidates Against Serogroup B
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                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              12510.1; -. 61917 MW; 4A3471514FD3C879 CRC64;
                                                                                                                                                                                                                                    01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0UTER MEMBRANE PROTEIN GNA992.
      Pred. No. 3.3e-179;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 174; DB 2; L
Pred. No. 5.9e-159;
0; Mismatches 1;
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                                                                                                                                                                                                                  592 AA
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Science 287:1816-1820(2000).
EMBL: AF226361; AAF42510.1; -
SEQUENCE 592 AA; 61917 WW; 4A3471514FD3C
                                                                                                                                                                                                                  PRT;
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100.08; Pre-
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Best Local Similarity 99.6
Matches 274; Conservative
                Conservative
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                                                                                                                                                                  334 OTGOADKFETVTSGT 348
                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                 QTGQADKFETVTSGT
       Similarity
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        Local
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                                                                                                                                                                                                                                  Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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Science 287:1816-1820(2000).
EMBL: AF226385; AAF42534 1. -
SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;
                                                 (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.9%; Score 171; DB 2; Le
100.0%; Pred. No. 4.7e-156;
iive 0; Mismatches 0;
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Bacteria; Proteobacteri
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SEQUENCE FROM N.A.
STRAIN-SWZ107;
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01-OCT-2000
01-MAR-2001
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01-DEC-2001 (TIEMBLIEL 19, Created)
01-DEC-2001 (TIEMBLIEL 19, Last sequence update)
01-DEC-2001 (TIEMBLIEL 19, Last annotation update)
01-DEC-2001 (TIEMBLIEL 19, Last annotation update)
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                                                                                01-DEC-2001 (TrEMBLrel. 19, NHHA OUTER MEMBRANE PROTEIN.
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Nature 404:502-506(2000).
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Q9JQW4
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                                                                                                                                                                                                                                                                                                                                                                                    108 ITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKE 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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Science 287:1816-1820(2000).

Science 287:1816-1820(2000).

SEQUENCE 590 AA, 61661 MW; 8AA476AC300D80C8 CRC64;
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.2%; Score 161; DB 2; Length 590; 100.0%; Pred. No. 2.1e-146; tive 0; Mismatches 0; Indels
                                                                                                                                                    Length 599;
                                                                                                                                                                                                     0; Indels
                                                      12513.1; -. 6C2E974AF7F78E9 CRC64;
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Last annotation update)
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                                                                                                                                                  28.9%; Score 171; DB 2; Le 100.0%; Pred. No. 4.7e-156; tive 0; Mismatches 0;
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Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
MEDE; AF226364; ARF42513.1; -
SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F
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01-007-2000 (TrEMBLrel. 15, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
0UTER MEMBRANE PROTEIN GNA992.
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Best Local Similarity
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STRAIN-EG327;

Bada II. Stikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;

"Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; ARTSG05, ARK6866.1; --

SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3ABEA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
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STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
Barbilla J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Jagels R., Lavis P., Devilin K., Feltwell T., Hamilin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quall M.A.,
Whitehead S., Spratt BG., Barrell BG.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423
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STRAIN=209900, BZ133, F6124, AND 22491;
MEDLINE-20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
Batti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Hudt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=65699, 487;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE SURRACE FIBRIL PROTEIN (OUTER MEMBRANE PROTEIN GNA992)
NMA1200 OR GNA992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

27.2%; Score 161; DB 2; Length 594
Best Local Similarity 100.0%; Pred. No. 2.1e-146;
Matches 161; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464
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Peak I.R., STIKhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Peak I.R., STIKhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR226368; AAR42517.1;
EMBL; AR2263368; ARA42507.1;
EMBL; AR226388; ARA42507.1;
                                                                                                                                                                                                                                                                                                                                                                                    354 KGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 413
                                                                                                                                                                                                                                                                                                                                                                                                           KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG 353
                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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MEDLINE-20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Comanducci C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffiles A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
                                                                                                                                                                                                                                         23.2%; Score 137; DB 16; Length 592; 100.0%; Pred. No. 2.9e-123; ive 0; Mismatches 0; Indels
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Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B Meniagococcus by Whole-Genome Sequencing.";
EMBLi AL162755; CAB84461.1;
EMBL; AL226357; AAF42506.1;
EMBL; AF226355; AAF42514.1;
EMBL; AF226373; AAF42514.1;
EMBL; AF226386; AAF42521;
EMBL; AF226386; AAF42521;
                                                                                                                                                                                      AD22E2F5EEF8F754 CRC64;
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ICE 594 AA; 62361 MW; 436BDDED68263C5C CRC64;
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100.0%; Pred. No. 5.8e-104;
tive 0; Mismatches 0;
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                                                                                                                                                                                    61745 MW;
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Best Local Similarity 100.(
Matches 137; Conservative
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Best Local Similarity 100.
Matches 117; Conservative
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SEQUENCE 592 AA;
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SEQUENCE FROM N.A.
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Q9JPH7
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176 TVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTAS 235
              236 DNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGK 292
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BASB029 amino acid
N. meningitidis EG
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A surface protein
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The invention provides proteins (AAY27201-245) from Neisseria meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis; bacterial infection; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New protein and its nucleotide sequence, useful in vaccines or diagnostic compositions for treating and/or preventing Neisseria meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of N. meningitidis protein ORF40-1.
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                                                                                                                                                                        AAY23745
AAU06173
AAY23738
AAU06178
AAB37830
AAU06181
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AAB37824
AAB37831
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AAU06183
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AAU06172
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                                AAU06174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 62; 123pp; English.
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98GB-0000760.
98GB-0019015.
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 (first entry)
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Neisseria meningitidis.
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W09936544-A2
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01-SEP-1998;
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AAY27202
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 Amino acid sequenc
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA191.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Score

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vaccine composition or a diagnostic composition. The composition is also useful for treating or preventing an infection due to Neisserial bacteria, especially Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                       79 EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS 138
                                                                                                                                                                                                                                                                                                                                             139 VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTN 198
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                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGY 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK 78
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                                                                                                                                                      Score 573; DB 20; Length 591;
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                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A surface protein of Neisserla meningitidis.
                                                                                                                                                 Query Match 97.0%; Score 573; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 573; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           559 SSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY23746 standard; Protein; 591 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                   The present sequence represents a surface protein of Neiserria menigitidis which is approximately 62 Kpa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerse, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis infection in humans. The N. meningitidis infection in humans prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to used to identify immunoreactive peptides.
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                                                                                                                                                                                                                            Neisseria meningitidis surface proteins useful for treating N.
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                                                                                                              Peak IRA;
                                       (ISIS-) ISIS INNOVATION LTD. (UYQU ) UNIV QUEENSLAND.
97GB-0026398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 573; Conservative
                                                                                                              Moxon ER,
                                                                                                                                                                                                                                                 meningitidis infections
                                                                                                                                                     WPI; 1999-418754/35.
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                                                                                                           Jennings MP,
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characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain PMC21 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                    the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are
                                                                                                   Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                       /note= "Predicted mature protein, specifically
  claimed in claim 12"
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/note= "Variable region 2"
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/note= "Conserved region
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/note= "Variable region
237..591
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/note= "Variable region
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|Tabel= Signal_peptide
                                                                                                                                                                                                                                            /label= Mature_NhhA
                                                                                                                      Neisseria meningitidis strain PMC21
                                                                                                                                          Location/Qualifiers
                     591 AA
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/note= "Conserved
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                    AAU06171 standard; Protein;
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N-PSDB; AAS09161.
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                                                           24-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                          378
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                                                                       Gaps
                                                                                                                                                                                                                                                                                            EGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTS
                                                                                                                                                                        VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK
                                                                                                                                                                                                                    VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTN
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                                          Length 591;
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                                                                     Indels
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                                          22;
                                          DB
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                                                                     Mismatches
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Pred. No.
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                              97.0%; Scor.
100.0%; Pre
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Protein;
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591
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                                                                    Matches 573;
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Sequence
                                         Query Match
Best Local S
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N. meningitidis EG329 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                    Surface antigen NhhA; meningococcal disease; meningitis vaccine.
 1..50
/label= Cl
'^ote= "Conserved region 1"
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/note= "Conserved region 3"
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/note= "Conserved region 2"
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/note= "Variable region 4"
237..591
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/note= "Variable region 2"
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                                                                                                                                                                                                              Neisseria meningitidis strain EG329.
                                                                                                                                                                                                                                          Location/Qualifiers
                                                                              AAU06175 standard; Protein; 591 AA
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N-PSDB; AAS09165.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 RIVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 YSLKKDLIDLISVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 TDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 VEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 NITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGN 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAP 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                  The present sequence represents a surface protein of Neiserria menightidis which is approximately 62 kDs. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans. The form of tacking the proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 LVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                     Neisseria meningitidis surface proteins useful for treating N. meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.8%; Score 525; DB 20; Length 591; 100.0%; Pred. No. 0; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                             Claim 1; Page 104-106; 132pp; English.
                                                                                                                                                                       Peak IRA;
                                                                            98WO-AU01031.
                                                                                                       97GB-0026398.
                                                                                                                               (ISIS-) ISIS INNOVATION LTD. (UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.0
es 525; Conservative
                                                                                                                                                                       Jennings MP, Moxon ER,
Neisseria meningitidis
                                                                                                                                                                                                WPI; 1999-418754/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                     591 AA;
                                                                                                                                                                                                            N-PSDB; AAX85793
                                                                                                     12-DEC-1997;
                                                                           14-DEC-1998;
                                                  24 - JUN - 1999.
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Best Local Si
Matches 525,
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in
New Nhh surface antigen polypeptides and polynucleotides from beisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Naisseria meningitidis -
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547 TYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591

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02-AUG-2001
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Protein
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       spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutent proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain E3329 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
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                                                                                                                                                         YSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 186
                                                                                                                                                                                                                                                                                                                           NITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGN 426
                                                                                                                                                                                                                                                                                                                                             nitvmydvnvgdalnvnglqnsgwnldskavagssgkvisgnvspskgkmdetvninagn 426
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therapeutic and prophylactic vaccines against a broader
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                                                                                                                                                                                                                              LVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Surface antigen NhhA; meningococcal disease; meningitis vaccine;
                                                                                                                               ö
                                                                                                            Length 591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                547 TYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
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                                                                                                                               Mismatches
                                                                                                                      o;
                                                                                                             Score 525;
Pred. No.
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis strain PMC21
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                                                                                                             88.8%,
100.0%; Pre-
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                                                                                                                      Best Local Similarity 100.
Matches 525; Conservative
                                                                    the present invention
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha meningitidis mutant polypeptides of the surface antigen Nhha charotterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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52..512
/label- Mature_NhhA_deletion_mutant_#1
/note= "Predicted mature protein, specifically
claimed in claim 12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen NhhA deletion mutant #1.
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                                                                                                                                                                                                                                    25-JAN-2001; 2001WO-AU00069
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                                                                                                                                                                                                                                                                                                                                                                                         Peak IRA, Jennings MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488774/53.
N-PSDB; AAS09172.
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359 TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE 418
                                                                                                                        TVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKP 478
                                                                                                                                                                                                    VRITHNVAPGVKEGDVTHVAQLKGVAQNLHNRIDHVDGNARAGIAQAIATAGLVQAYLPGK 538
                                                                                                                                                                                                                                                                        The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                 240 dfvrtydtveflsadtktttvnveskdngkktevkigvktsvikekdgklvtgkdkgeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Surface antigen NhhA; meningococcal disease; meningitis vaccine; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /libbl- Signal_peptide
52..433
/label- Mature_Nhha_deletion_mutant_#3
/note= "Predicted mature protein, specifically
claimed in claim 12"
                                                                                                                                                                                                                                                                                                                                              539 SMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N. meningitidis PMC21 NhhA deletion mutant #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis strain PMC21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU06185 standard; Protein; 433 AA
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N-PSDB; AAS09175.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 DLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 dlyldpvqrtvavlivnsdkegtgekekveensdwavyfnekgvltareitlkagdnlki 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 KONGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a surface protein of Neiserria menigitidis which is approximately 62 kDs. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20; Length 592;
                                                                                                                                                                                                                                                                                    Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
          A surface protein of Neisseria meningitidis.
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99.8%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 86-87; 132pp; English.
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                                                                                                                                       AAY23737 standard; Protein; 592
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les 532; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jennings MP, Moxon ER,
                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis.
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Best Local Si
Matches 532;
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diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface antigen Nhha deletion mutant #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.
                                                                                                                                   EVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTAN 330
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                                                                                                                                                                                                                                                                                                      RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKT 270
                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                            DNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIK
                                                                                                                                                                                                                            NLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSV
                                                                                                                                                                                                                                                            SLGAGADAPILSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRI
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                                                                                           Length 433;
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                                                                                          22;
                                                                                     64.5%; Score 100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                            GTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                                                    413 gtasgnsrghfgasasvgygw 433
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                        Matches 381; Conservative
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Misc-difference 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
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                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 92
                                                                 433 AA;
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                                                                 Sequence
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particularly genetic immunisation. Antibodies against PASB029 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism receiving the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serogroup B strain H4476. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and polypeptide sequences (AAZ5044-YZ7045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is usecful in the diagnosis of the stage of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 NFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIG 183
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                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the Nisseria meningitidis BASB029 amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 367; DF
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0; Mismatches
CGT
                                                                                                                                                                                                                                      SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
/note= "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Fig 2; 74pp; English
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99.8%;
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467; Conservative
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                                                                                                                                           07-MAY-1999;
                                                                                                                                                                                         13-MAY-1998;
                                                                                           18-NOV-1999.
                                                                                                                                                                                                                                                                                         Ruelle J;
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Matches 46
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Matches 355; Conservative
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                or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Surface antigen NhhA; meningococcal disease; meningitis vaccine; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..51
/label- Signal_peptide
52..407
/label- Mature_NhhA_deletion_mutant_#2
/note= "Predicted mature protein, specifically
claimed in claim 12"
                                                                                                          N. meningitidis PMC21 NhhA deletion mutant #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis strain PMC21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                            AAU06184 standard; Protein; 407 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001; 2001WO-AU00069
                                                                                                                                                                                                                                                                                                                                                                      24-OCT-2001 (first entry)
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N-PSDB; AAS09174.
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60.1%; Score 355; DB 22; Length 407; 100.0%; Pred. No. 0;

Query Match Best Local Similarity

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237 NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGE 296
                                                                                                                                                 NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGT 356
                                                               357 TATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKM 416
                                                                                                               477 KPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLP 536
                                                                                                                                                                                                                  New Nhha surface antigen polypeptides and polynucleotides from besseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the isolation of novel Neisseria
                                                                                                                                                                                                                                                                  537 GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                                                                                                                                                      Surface antigen NhhA; meningococcal disease; meningitis vaccine; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.09

/label= Signal_peptide

50..50

/label= Mature_NhhA_deletion_mutant_#4

/note= "Predicted mature protein, specifically

claimed in claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                    N. meningitidis PMC21 NhhA deletion mutant #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis strain PMC21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                         AAU06186 standard; Protein; 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 9; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2000; 2000US-0177917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2001; 2001WO-AU00069.
                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peak IRA, Jennings MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488774/53.
N-PSDB; AAS09176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200155182-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                  AAU06186;
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New protein and its nucleotide sequence,
WPI; 1999-444400/37.
N-PSDB; AAX99123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jennings MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9931132-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                             08-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUN-1999.
                                                                                                                                                                                                          Best Local Sim
Matches 175;
                                                                                                                                                                                                                                                                                                                                                                                                           AAY23740;
                                                                                                                                                                     Sequence
                                                                                                                                                                                                Query Match
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      (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PWC21 surface antigen NhhA deletion mutant #4.
                                                                                                                                                                                                                                                                             NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGT 356
                                                                                                                                                                                                                                        TATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKM 416
                                                                                                                                                                                                                                                                                                           DETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDN 476
                                                                                                                                                                                                                                                                                                                    477 KPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLP 536
                                                                                                                                                                                      NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGE 296
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                        GKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
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 meningitidis mutant polypeptides of the surface antigen NhhA
                                                                                                                                               DB 22; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scarlato V;
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of N. meningitidis protein ORF40.
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                                                                                                                                               60.1%; Score 355; DB
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY27201 standard; Protein; 245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masignani V, Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-0022143.
98GB-0000760.
98GB-0019015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-IB00103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                        Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR-) CHIRON SPA.
                                                                                                                   502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JAN-1999;
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14-JAN-1998;
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                                                                                                                                                         Local Sim.
hes 355;
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                                                                                                                                               Query Match
Best Local S:
Matches 355,
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                                                                                                                   Sequence
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                                                                                                                                      The invention provides proteins (AAY27201-245) from Neisseria meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition or a diagnostic composition. The composition is also bacteria, especially Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 TNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 KAGDNLKIKONGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKD 285
leotide sequence, useful in vaccines or for treating and/or preventing Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis surface proteins useful for treating N.
                                                                                                                                                                                                                                                                                                                                                                                                          Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Surface protein; surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 7.7e-169;
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 175; DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 100-101; 132pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
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                                                                                                                                                                                                                                                                                                                                                                                                             29.00.
100.0%; Pre-
                                                                                           Claim 1; Page 61; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY23740 standard; Protein; 594
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                                                                                                                                                                                                                                                                                                                                                                                                          29.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS INNOVATION (UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moxon ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              meningitidis infections
                        diagnostic compositions
                                            meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoreactive peptide.
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N-PSDB; AAX85792.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                     245 AA;
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polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments. BASB039 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB039 polypeptides and polypeptides are useful for generating an Immune response in an animal. A therapeutic composition comprising an antibody directed against BASB039 is useful in treating humans with Neisseria meningitidis disease. The polynuclectide is useful in treating humans with Neisseria in fection which results from increased or decreased expression of the polynuclectide, and for therapeutic or prophylactic purposes, polynuclectide, and for therapeutic or prophylactic purposes, polynuclectide, and for therapeutic or prophylactic purposes, polynuclectides and polypeptides are also useful for treating infections particularly genetic immunisation. Antibodies against BASB029 polynuclearide and development of antibacterial drugs. Bused recombinant protein is useful for the stimulation of the immune system of an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= v2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Vl
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                      receiving the protein.
                                                                                                                                                                                                                                                                                                          594 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU06174;
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.
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                                                                                                                                                                                                                                                                                                        304 GEGLUTAKEVIDAVNKAGWRMTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 363
                                                                                                                                                                                                                                                                                                                             364 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain ATCL1300. The BASB029 protein is homologous to Haemophilus influences surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and
    The present sequence represents a surface protein of Neiserria menigitidis which is approximately 62 kDs. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerses, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans. The the form of vaccines. The proteins and antibodies can also be used to used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                     Length 594;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 466
                                                                                                                                                                                                                                                                                                                                                                                                                                               424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464
                                                                                                                                                                                                                                 Match 27.2%; Score 161; DB 20; L. Local Similarity 100.0%; Pred. No. 2.9e-154; es 161; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by AATC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers Misc-difference 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY57044 standard; Protein; 594 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-053103/04.
                                                                                                                                                                                  594 AA;
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                                                                                                                                                                                    Sednence
                                                                                                                                                                                                                                     Query Match
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                                                        364 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423
                                                                                                  304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 363
                    0; Gaps
                                                                                                                                                                                                                                                                            N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                Surface antigen NhhA; meningococcal disease; meningitis vaccine
 Length 594;
                    0; Indels
                                                                                                                                424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464
                                                                                                                                             27.2%; Score 161; DB 21; I
100.0%; Pred. No. 2.9e-154;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            /label= C1
/note= "Conserved region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= C4
/note= "Conserved region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= C2
/note= "Conserved region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= C3
/note= "Conserved region 3"
                                                                                                                                                                                                                                                                                                                                                                                                           "Variable region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= V3
/note= "Variable region 3"
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                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis strain EG327.
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                           AAU06174 standard; Protein; 594 AA
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhA (AMU06182-AAU06186). The modified or mutant NhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylatcic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen. The present sequence representing the wild type surface antigen NhA (AMU06171-AAU06180) from 10 different N. meningitidis strains given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                   New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
232..238
/label= V4
/note= "Variable region 4"
239..594
/note= "Conserved region 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Fig 1; 91pp; English
                                                                                                                                                                                             25-JAN-2001; 2001WO-AU00069.
                                                                                                                                                                                                                             25-JAN-2000; 2000US-0177917
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; 0 304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 363 364 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423 Gaps 0 27.2%; Score 161; DB 22; Length 594; 100.0%; Pred. No. 2.9e-154; Live 0; Mismatches 0; Indels ( Best Local Similarity 100. Matches 161; Conservative ŏ a ò qq ò

Query Match

AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464 424

Search completed: September 5, 2002, 10:40:44 Job time: 451 sec

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Result Š

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Sequence 21, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JEANINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 65564/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: CT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-14
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21
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ENGTH: 591
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US-09-669-974-11
US-09-669-974-2
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US-09-669-974-7
US-09-377-155-7
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                                                             GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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    protein search, using sw model

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Sequence Sequence Sequence

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-09-377-155-5 US-09-669-974-5

ALIGNMENTS

RESULT 1 US-09-377-155-21

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Conservative
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: WOXON, E. Richard
TITLE OF INVERTION.
FILE REPERENCE: 06504/0128
CURRENT APPLICATION NUMBER: US/09/669, 974
CURRENT FILING DATE: 2000-09-26
FRIOR PPLICATION NUMBER: US/09/71/155
PRIOR PELICATION NUMBER: D99-08-19
PRIOR PELICATION NUMBER: PGT/AU98/01031
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1998-12-14
SRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
SOSTWARE: PATENTING DATE: 1997-12-12
SOSTWARE: PATENTING DATE: 1997-12-12
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APPLICANT: MOXON, En Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.0
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CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
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SEQ ID NO 2
LENGTH: 592
                            TYPE: PRT
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100.0%; Pred. No. 0;
:ive 0; Mismatches
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALCHIN VET. 2.0
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Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PATENTIN VEr. 2.0
; SEQ ID NO 11
; LENGTH: 591
                                                                                                         TYPE: PRT CRGANISM: Neisseria meningitidis US-09-669-974-11
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Matches 525; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: WOXON, E. Richard
ITILE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1999-08-19
PRIOR PILING DATE: 1999-08-19
SOFTWARE: PATENTION NUMBER: CB 9726398.2
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VOFT. 2.0
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                                                                                           Score 432;
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; ORGANISM: Neisseria meningitidis US-09-377-155-2
                                                                                      73.1%;
99.8%;
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Matches 532;
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LENGTH: 592
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REPERBACE: 06504/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR PLILING DATE: 1998-12-14
PRIOR PLILING DATE: 1998-12-14
PRIOR PLILING DATE: 1998-12-12
PRIOR FILING DATE: 1998-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEC ID NOS: 33
SOFTWARE: PATCHILING DATE: 1997-12-12
                                                                                                                                                                                                                                                                           Sequence 9, Application US/09669974; Patent No. 6333173; GENERAL INFORMATION:
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US-09-669-974-9
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73.1%; Score 432; DB 4; Length 592;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 532; Conservative 0; Mismatches 1; Indels
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065.064/012
CURRENT FILING DATE: 1999-08-19
PRIOR PILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: 05.7/4U98/01031
PRIOR PILING DATE: 1999-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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; ORGANISM: Neisseria meningitidis
US-09-377-155-9
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                                                          0; Gaps
   Length 594;
                                                      0; Indels
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Ouery Match 27.2%; Score 161; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 3.5e-144;
Matches 161; Conservative 0; Mismatches 0;
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APPLICANT: PEAK, Ian Richard Paul
APPLICANT: PEAK, Ian Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 05604/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-18-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR PRILING DATE: 1998-12-14
PRIOR PRILING DATE: 1998-12-14
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; Patent No. 6197312
; GENERAL INFORMATION:
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APPLICATION NUMBER: PCT/AU98/01031
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US-09-377-155-15
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LENGTH: 598
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Sequence 13, Application US/09377155
Fatent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: JONON, E. Richard TITLE OF INVENTION: NOVEL SUFFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669, 974
CURRENT PILLING DATE: 1999-08-19
PRIOR FILLING DATE: 1999-08-19
PRIOR FILLING DATE: 1999-101-14
PRIOR FILLING DATE: 1999-12-12
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CURRENT FILING DATE: 1999-08-19
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US-09-669-974-7
                                                      TYPE: PRT
ORGANISM: Neisseria meningitidis
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SOFTWARE: PatentIn Ver. 2.0
 PatentIn Ver.
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SOFTWARE:
SEQ ID NO 7
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SEQ ID NOS: 33
SEQ ID NOS: 33
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
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; Patent No. 6197312
                                                                                                                                                                                                                                 ; ORGANISM: Neisseria meningitidis US-09-377-155-13
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; ORGANISM: Neisseria meningitidis
US-09-669-974-13
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APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILENG DATE: 1999-08-19
CURRENT FILING DATE: 1999-08-19
PRIOR PELICATION NUMBER: CT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
NUMBER OF SEQ ID NOS: 33
SOCTHWARE: PATCHIN DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 15
LENGTH: 599
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APPLICANT: PERK, I EN RICHARD ANSELM
APPLICANT: PERK, I EN RICHARD ANSELM
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON E. Richard
TITLE OF INVENTION NOVEL SURFACE ANTIGEN
FILE REPERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: US/09/7377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-102-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOSE: 33
SOFTWARE: PATECHTIN VOYET: 2.0
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; ORGANISM: Neisseria meningitidis
US-09-669-974-15
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US-09-669-974-15
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RESULT 15 US-09-377-155-17

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; Sequence 17, Application US/09377155
; Patent No. (5197312);
; GENERAL INFORMATION:
APPLICANT: DENNINGS, Michael Paul
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXOW. E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REPERENCE: 050604/0128
CURRENT APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
PRIOR FILING DATE: 1998-12-14
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PRIOR PRI
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C. Accession: G81133
R. Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A. A. Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A. A. Accession: G81133
A. Accession: G81133
A. Status: preliminary
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-591 < TETS
A. Cross-references: GB: AE002450; GB: AE002098; NID: 97226229; PIDN: AAF41395.1; PID: 9722623
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C,Genetics:
A,Gene: NMB0992
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1675.186 Million cell updates/sec
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probable surface f
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C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                      Compugen Ltd.
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GenCore
Copyright (c) 1993
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                                                                                        protein search, using
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Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
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137
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probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z probate: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 (A propagation of A parts of A part
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A;Experimental source: serogroup A, strain 22491
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                                                                                                                           19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK
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100.0%; Pred. No. 1.8e-133
iive 0; Mismatches 0;
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A;Gene: NMA1200
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294 KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG 353
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	414 GKMDETVNINAGNNIEI 430 	414	Qy Dp
413	354 KGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 413	354	qq
413	354 KGTTATVSKDDGGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 413	354	ζŏ

Search completed: September 5, 2002, 10:41:54 Job time: 220 sec

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

September 5, 2002, 10:48:19 ; Search time 19.15 Seconds
(without alignments)
1194.948 Million cell updates/sec

US-09-700-293-4 591 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASASVGYQW 591

Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

105224 seqs, 38719550 residues Searched:

. 20 Word size :

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description 8 tesult Query No. Score Match Length DB Result

No matches found

Search completed: September 5, 2002, 10:48:19 Job time: 420 sec

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Thu Sep

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September 5, 2002, 10:47:55 ; Search time 55.95 Seconds
(without alignments)
1827.346 Million cell updates/sec
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1 MNKIYRIIWNSALNAWVAVS.....TASGNSRGHFGASASVGYQW 591
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                 562222 seqs, 172994929 residues
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Gapop 60.0 , Gapext 60.0
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Perfect score:
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26

Total number of hits satisfying chosen parameters:

summaries

Post-processing: Listing first 1000

SPTREMBL\_19:\*

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000 1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fung:\*
4: sp\_fung:\*
5: sp\_lnvertebrate:\*
6: sp\_mammal:\*
7: sp\_mc:\*
8: sp\_phage:\*
9: sp\_phage:\*
11: sp\_rodent:\*
12: sp\_virus:\*
13: sp\_virus:\*
14: sp\_archeap:\*
15: sp\_archiap:\*
16: sp\_archeap:\*
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

 Result
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 Description

 No.
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 Description

 1
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 09Jps7 neisseria m

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 09Jps7 neisseria m

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 09ADF4
 09Jps4 neisseria m

 5
 220
 37.2
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 09JPS4
 09Jps1 neisseria m

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 174
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## ALIGNMENTS

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Science 287:1816-1820(2000).
EMBL, AF226366; AAR4215.1; .
SEQUENCE 591 AA, 62113 WW; 533453CAE5A91BIF CRC64;
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                                                                                                                                                                                       STRAIN-BZ147;
MEDLINE-20175756; PubMed-10710308;
Pizza M. Scarlato V., Masignan V., Giuliani M.M., Arico' B.,
Pizza M. Scarlato V., Masignan V., Giuliani M.M., Arico' B.,
Pizza M. Scarlato V., Masignan V., Giuliani M.M., Arico' B.,
Gomanducci M., Jennings G.T., Baldi L., Barchini E., Capecchi B.,
Galectti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nutti S.,
Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Brock D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon B.R., Grandi G., Rappuoli R.,
"Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                          19 VSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK 78
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                                                                                                                    o;
                                                                   Score 573; DB 16; Length 591;
Pred. No. 0;
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  591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;
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0.09DFS7;

0.1-0CT-2000 (TrEMBLrel. 15, Last sequence update)

01-0CT-2000 (TrEMBLrel. 15, Last sequence update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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SIRAIN=E6329;
John Strain Stra
                                                                                                                                                                                                                                                                                                                                                    96 YFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNI 155
                                                                                                                                                                                                                                                                                                                                                                                                       TSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASV 215
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                                                                                                                                                                                                                Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                                                                                           ;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NHHA OUTER MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 AA
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Bacteria; Proteobacteri
NCBI_TaxID=487;
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SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Mocon E.R., Grandi G., Rappuoli R.; Maneti B., Grandi G., Rappuoli R.; "Identification of Vaccine Candidates Against Serogroup B
  SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
                                                                                                                                                                                                                                                                                                                                                                                         TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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MEDLINE-20175756; Pubmed-10710308;
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tes 220; Conserv
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SEQUENCE FROM N.A.
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
"Identification and characterisation of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF125375; AAK09243.1; -.
SEOUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;
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                                                                                                   RTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFT 126
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                                                     Gaps
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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  Length 591;
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88.8%; Score 525; 100.0%; Pred. No.
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
OUTER MEMBRANE PROTEIN.
NHHA.
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Best Local Similarity 100.0
Matches 195; Conservative
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SEQUENCE FROM N.A.
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                         09JP13 PRELIMINARY; PRT; 594 AA.
09JP13; Capural
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01TBR MEMBRANE PROTEIN GNA992.
GNA992.
Bucieria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_PAXID=487;
         492 DVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGE 551
                                                                                                                                                                                                                                                      Bacteria; Proteóbacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=487;
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EMBL; AF225380; AAR425291; -
SEQUENCE 530 AA; 55190 MW; 1F836CA57598515B CRC64;
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                                                                                                                                                                          487 AGYALGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 526
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                                                            552 AGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                       530 AA
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Matches 220; Conservative
                                                                                                                                                     PRELIMINARY;
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SEQUENCE FROM N.A.
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152 KVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKR 211
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NCBI_TaxID=487;
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                                                          Pizza M., Scallato V., Masignani V., Giuliani M.M., Arico' B., Pizza M., Scallato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galoctti C.L., Luzzi E., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zon M. Nuti S. Broeker M., Hudd E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.; Moxon E.R., Grandi G., Rappuoli R.; Moxon E.R., Grandi G., Rappuoli R.; Science 287:1861-1820(2000).
Science 287:1816-1820(2000).
EMBL, AF226376; AAF42218.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.0%; Score 195; DB 2; Length 594; 100.0%; Pred. No. 3.3e-179; tive 0; Mismatches 0; Indels
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"Identification of Vaccine Candidates Against Serogroup B
Menhigococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000)
EMBL; AF226379; AAF42528.1;
SEQUENCE 594 AA; 62114 WW; 1E2A63A78F53D256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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STRAIN=NG3/88, AND BZ232;
MEDLINE=20175756; PubMed=10710308;
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MEDLINE-20175756; PubMed-10710308;
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Best Local Similarity 100.0
Matches 195; Conservative
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         KVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKR
                                                     AASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTE
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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STRAIN-860800;
MEDLINE-20175756; PubMed=10710308;
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                                                                                                                                                332 QTGQADKFETVTSGT 346
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Bacteria; Proteobacteri
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354 KGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 413
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole Genome Sequencing.";
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SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;
                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 171; DB 2; Le
Pred. No. 4.7e-156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                       STRAIN=SWZ107;
MEDLINE=20175756; Pubmed=10710308;
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MEDLINE=20175756; Pubmed=10710308;
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100.0%; Pre
0, )
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                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=487;
                                                                                                                                                                                 NCBI_TaxID=487;
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Best Local Simi
Matches 171;
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                  Q9JPR7
                                                                                                                      GNA992
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09JPS8
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Gaps

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STRAIN-EG327;
SIKhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Plack I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF157605; AAK688661; "9DDD48B04B3A8EA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STAIN-22491 / SERGROUP A / SERCTYPE 4A;
MEDLINE-202555; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Fark S.R., Morelll G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Walandream M.A., Rutherford K.M., Shimonds M., Skelton J.,
Whitchnead S., Spratt B.(6., Barrell B.G.);
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 363
                                                                                                                                                                                              Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis (serogroup A), and
Maisseria meningitidis.
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TAXID=65699, 487;
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STRAIN-205900, BZ133, F6124, AND 22491;
MEDLINE-20175756; Pubmed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Comanducci M., Jennings G.T., Manetti R., Marchetti E., Mora M., Nuti S.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Moxon E.R., Grandi G., Rappuoli R.;
Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE SURRACE FIBRIL PROTEIN (OUTER MEMBRANE PROTEIN GNA992).
NMA1200 OR GNA992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.2%; Score 161; DB 2; Length 594; 100.0%; Pred. No. 2.1e-146; Live 0; Mismatches 0; Indels
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLRel. 19, Last annotation update)
NHH OUTER MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464
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Matches 161; Conservative
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                                                                                                                                                      Neisseria meningitidis
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  NCBI_TaxID=487;
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    δy
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                                                                                                                                                                                                                                                                                                                                            294 KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 KGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 TAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 ITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 TAGINGDITVHLNGIGSTLIDTLLNTGATINVINDNVIDDEKKRAASVKDVLNAGWNIKG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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MEDLINE-SQT15756; PubMed=10710308;
MEDLINE-SQT15756; PubMed=10710308;
MEDLINE-SQT15756; PubMed=10710308;
Comanducci M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Canedocti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Rati G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 471
                                                                                                                                                      Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 590;
                                                                                                                                              Ouery Match 28.9%; Score 171; DB 2; Length 59 Best Local Similarity 100.0%; Pred. No. 4.7e-156; Matches 171; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
EMBL; AF226364; AAF42513.1; -.
SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;
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61661 MW; 8AA476AC300D80C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 VKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 27.2%; Score 161; DB 2; Le Local Similarity 10.0%; Pred. No. 2.1e-146; Des 161; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           594 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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MEMBRANE PROTEIN GNA992.
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SEQUENCE 590 AA; 61661
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Best Local S
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Q9JPS3;
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09JPS3 11
09JPS3 11
01-07E 09JPS3 12
07 09JPS3 
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Q93QY4
ID Q93QY4
AC Q93QY4
DT 01-DEC
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL. AFZ26368, AAF42517.1;
                                                                                                                                                                                                                                                                                                                  354 KGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 413
                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 19, Last annotation update)
001-DEC-2001 (TREMBLRel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GNA992 OR NHHA.
Neisseria meningitidis.
Bacteria: Proteobacteria: beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                   294 KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG 353
                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                    Length 592;
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                                                                                                                                                                                                                 Indels
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AF157604; AAK68865.1; -...
NCE 594 AA; 62361 MW; 436BDDED68263C5C CRC64;
                                                                                                                               592 AA; 61745 MW; AD22E2F5EEF8F754 CRC64;
                                                                                                                                                                                23.2%; Score 137; DB 16; I 100.0%; Pred. No. 2.9e-123; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 AA.
Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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MEDLINE-20175756; PubMed-10710308;
            Science 287:1816-1820(2000).
EMBL, AL16775; CAB84461.1; -
EMBL, AF226357; AAF42566.1; -
EMBL, AF226355; AAF42514.1; -
EMBL; AF226313; AAF42522.1; -
EMBL; AF226386; AAF42535.1; -
                                                                                                                                                                                                                                                                                                                                                                                                       414 GKMDETVNINAGNNIEI 430
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Best Local Similarity 100.0
Matches 137; Conservative
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SEQUENCE FROM N.A.
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Search completed: September 5, 2002, 10:47:57 Job time: 428 sec

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1123.218 Million cell updates/sec
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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10	161	27.1		20	AAY23746	A surface protein

The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 KDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for

Neisseria meningitidis surface proteins useful for treating N.

Claim 1; Page 100-101; 132pp; English.

meningitidis infections

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			27.1	591	77	AAU06175	itidis
		61 28	~ ~	592	20	AAY23737	
		38	3	583	20	AAY23745	surface protei
	۲ a	3 38	mr	589 100	22	AAU06173 AAV23744	N. meningitidis P2
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SO.	Neisseria		meningitidi	idis.			
X A	W099311	132-A1.					
X	WIT - AC	0001					
g X	200	1222					
PF	14 - DEC	-1998;	98W	98WO-AU0103	331.		
PR	12-DEC	-1997;	9761	97GB-0026	398.		
A P P	(ISIS- (UYQU	-) ISIS ( ) UNIV	INNOVATION QUEENSLAND		LTD.		
PI	Jenning	gs MP,	Moxon	n ER,	Peak	k IRA;	
DR DR	WPI; 19 N-PSDB;	O1	9-418754/3: AAX85792.	5.			

99WO-EP03255. 98GB-0010276

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New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
                                                                                 (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                    Claim 4; Fig 2; 74pp; English.
                                                                                                                         WPI; 2000-053103/04.
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                                                                                                               Gaps
                                                                                                                                            1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTDDDDLYLE 60
the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
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0
                                                                                         Query Match

100.09; Score 594; DB 20; Length 594;
Best Local Similarity 100.08; Pred. No. 0;
Matches 594; Conservative 0; Mismatches 0; Indels 0;
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Misc-difference 104
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This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain ATCC13090. The BASB029 protein is homologous to the serogroup B strain ATCC13090. The BASB029 protein. The invention relates to BASB029 polyunclectide sequences (AAZ39664-239865) and polypeptide sequences (AAZ39664-39664-239865) and polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polypeptides are useful for generating an Immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in treating humans with Neisseria in the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 particularly bacterial infections. The protein is useful in the strenged and development of antibacterial drugs. Fused recombinant receiving the protein.
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                                                                                                                                                          Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                              N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
                                                                       541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
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/note= "Conserved region 5"
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/note= "Variable region
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/note= "Conserved
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain 63327 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH 180
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                      Neisseria meningitidis; useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
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NhhA surface antigen polypeptides and polynucleotides from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   594;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                Claim 9; Fig 1; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 594; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 AA;
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigon NhhA (AAUG6186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in alganostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface antigen NhhA deletion mutant #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Nhha surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                          Surface antigen NhhA; meningococcal disease; meningitis vaccine; mutein.
                                                                                                                                                                                                                                                                                                                                                                           52..433 /
/label- Mature NhhA_deletion_mutant_#3
/note= "Predicted mature protein, specifically
claimed in claim 12"
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                                                                                                                                                         N. meningitidis PMC21 NhhA deletion mutant #3.
                                                                                                                                                                                                                                                                                                                                                                /label= Signal_peptide
                                                                                                                                                                                                                                                           Neisseria meningitidis strain PMC21.
Synthetic.
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                     AAU06185 standard; Protein; 433 AA.
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                                                                                                                      (first entry)
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N-PSDB; AAS09175.
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                                                                                                                    24-OCT-2001
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                                                                            AAU06185;
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Best Local S
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                AAU06185
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
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                                                                                             Surface antigen NhhA; meningococcal disease; meningitis vaccine; mutant; mutein.
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                                                     N. meningitidis PMC21 NhhA deletion mutant #2.
                                                                                                                                                                                                                                                           /label= Signal_peptide
                                                                                                                                                       Neisseria meningitidis strain PMC21
                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2001; 2001WO-AU00069.
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                (first entry)
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N-PSDB; AAS09174.
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Matches 161;
                                                                                                                                                                            Synthetic.
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                                                     306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                                     366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
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Length 433;
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215 geglvtakevidavnkagwrmktttangqtgqadkfetvtsgtnvtfasgkgttatvskd 274
                                                                             DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                     426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
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AAU06182
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206 daganitymydynnygdalnynglqnsgwnldskavagssgkvisgnyspskykmdetynin 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                        Surface antigen NhhA; meningococcal disease; meningitis vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mature NhhA deletion_mutant_#4
"Predicted mature protein, specifically
claimed in claim 12"
                                                AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
                                                                                                                                                                                                                                                                                                                                                                                     N. meningitidis PMC21 NhhA deletion mutant #4.
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                                                                                                                                                                                                                          AAU06186 standard; Protein; 502
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/label= N
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N-PSDB; AAS09176.
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence represents N. meningitidis strain PMC21 surface antigen NhAA deletion mutant #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Surface antigen NhhA; meningococcal disease; meningitis vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                            N. meningitidis PMC21 NhhA deletion mutant #1.
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/label= Signal_peptide
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N-PSDB; AAS09172.
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                                                                                                                                                                                                                                                                                     NAME OF COLOR OF STREET STATES OF STREET
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Length 502; Indels

Score 161; DB 22; L Pred. No. 1.3e-149;

Best Local Similarity 100. Matches 161; Conservative

Query Match

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304 geglvtakevidavnkagwrmktttangqtgqadkfetvtsgtnvtfasgkgttatvskd 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitidis which is approximately 62 kms. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis surface proteins useful for treating N. meningitidis infections
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                                                                                                                                                                                                                                                                                                                                                                                Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.
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                                                                                              426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
                                                                                                                  424 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.1%; Score 161; DB 20; L 101 100.0%; Pred, No. 1.5e-149; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                           A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 104-106; 132pp; English.
                                                                                                                                                                                                                               Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peak IRA;
                                                                                                                                                                                                                           AAY23741 standard; Protein; 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-AU01031.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moxon ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                591 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09931132-A1
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Matches 161;
                                                                                                                                                                                                                                                                  AAY23741;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides proteins (AAY27201-245) from Neisseria menigitidis (strains A and B) and nucleic acid sequences (AAX99123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition and adjancestic composition. The composition is also useful for treating or preventing an infection due to Neisserial bacteria, especially Neisseria meningitidis.
                                                                        306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                                                              366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                                                                                        285 dqgnitvmydvnvgdalnvnglqnsgwnldskavagssgkvisgnvspskgkmdetvnin 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis; bacterial infection; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New protein and its nucleotide sequence, useful in vaccines or diagnostic compositions for treating and/or preventing Neisseria meningitidis infections
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  Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.1%; Score 161; DB 20; Length 591; 100.0%; Pred. No. 1.5e-149; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scarlato V;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of N. meningitidis protein ORF40-1.
                                                                                                                                                                                                                           426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
                                                                                                                                                                                                                                            27.1%; Score 161; DB 22; L
100.0%; Pred. No. 1.3e-149;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                          AAY27202 standard; Protein; 591 AA.
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98GB-0000760.
98GB-0019015.
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                                     Matches 161; Conservative
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                 Similarity
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Matches 161; Conserv
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  Query Match
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QY Db

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BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; Infection; treatment; prevent; antibacterial drug.
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                                                         BASB029 amino acid sequence from N. meningitidis strain H44/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                ^{\sim_I} Location/Qualifiers Misc-difference 90
                                                                                                                             Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-053103/04.
                                                                                                                                                                                                                                                       Misc-difference 108
                                                                                                                                                                                                                                                                                   Misc-difference 123
                                                                                                                                                                                                                                                                                                               Misc-difference 269
                                                                                                                                                                                                 Misc-difference 92
                                                                                                                                                                                                                             Misc-difference 98
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                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                             21-FEB-2000
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 AAY57045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 KDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                                                Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.
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100.0%; Pred. No. 1.5e-149;
ive 0; Mismatches 0;
                                                                                                                                                         A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 127-128; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY57045 standard; Protein; 591 AA.
                                                                   AAY23746 standard; Protein; 591 AA
                                                                                                                                                                                                                                                                                                                                                                                                                Peak IRA;
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                                                                                                                             (first entry)
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Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Jennings MP, Moxon ER,
                                                                                                                                                                                                                             Neisseria meningitidis.
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Best Local Similarity
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ID AAY57
                                                         AAY23746
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98GB-0010276.

by AAC"

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'note= "Encoded by AAT"

(first entry)

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This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain H44/76. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polymcleotide sequences (AAZ39864-Z39865) and polypeptide sequences (AAX57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, ausceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           particularly genetic immunisation. Antibodies against BASB029 polynuclectides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism
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Claim 4; Fig 2; 74pp; English.
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New Nhh, surface antigen polypeptides and polynucleotides from besseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                          Claim 9; Fig 1; 91pp; English.
       Peak IRA, Jennings MP;
                     WPI; 2001-488774/53.
                              N-PSDB; AAS09161.
                                                                                                                                                                                                                                                                                                                                                                                         AAU06175;
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                                                     306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                      366 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
Gaps
                                                                                                                                                                          N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                        Surface antigen NhhA; meningococcal disease; meningitis vaccine.
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                                                                                                                                                                                                                                                                                    /note= "Predicted mature protein, specifically claimed in claim 12"
Indels
                                                                         426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
                                                                                   424 agnnieitrngknidiatsmtpqfssvslgagadaptlsvd 464
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/note= "Conserved region 1"
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Mismatches
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                                                                                                                                                                                                                                   /label- Signal_peptide
                                                                                                                                                                                                       Neisseria meningitidis strain PMC21.
                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                             AAU06171 standard; Protein; 591 AA.
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                                                                                                                                                          24-OCT-2001 (first entry)
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Matches 161; Conservative
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                                                                                                                                            AAU06171;
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigon NhhA (AAU06187-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strains pMC21 is 1 of 10 NhhA polypeptide sequences (AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.1%; Score 161; DB 22; Length 591; 100.0%; Pred. No. 1.5e-149; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //label= C2
/note= "Conserved region 2"
121..124
/label= V2
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/label= Cl
/note= "Conserved region 1"
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/note= "Variable region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis strain EG329
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Matches 161; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            the present invention.
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AAY23737 standard; Protein; 592 AA.
RESULT 14
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               AAY23737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen. NhA ANU06186. The modified or mutant NhIA polypeptides are characterised by deletions of non-conserved amino edids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain 63329 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
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100.0%; Pred. No. 1.5e-149
iive 0; Mismatches 0;
 /nove
125..18
/label= C3
'~^te= "Conserved region 3"
                                                                                                           //11.....
/label= C4
/note= "Conserved region 4"
                                                                                                                                                                                                                           /note= "Conserved region 5"
"Variable region 2"
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                                                                                                                                                 /label= V4
/note= "Variable region
237..591
                                                                       label= v3
'note= "Variable
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161; Conservative
                                                                                                     211..229
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                                                                                                                                                                                                                                                                                                                                                                                                              Jennings MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488774/53.
N-PSDB; AAS09165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           591 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         meningitidis which is approximately 62 kps. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence represents a surface protein of Neiserria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis surface proteins useful for treating meningitidis infections
                                                                                                                                surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 161; DB 20; I
Pred. No. 1.5e-149;
0; Mismatches 0;
                                                                                     A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 86-87; 132pp; English
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100.0%; Pic
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                                                                                                                                                                                                                                                                                                                               98WO-AU01031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moxon ER,
                                                                                                                                                    immunoreactive peptide
                                                                                                                                                                                               Neisseria meningitidis
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                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX85788
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                                                                                                                                                                                                                                                                                                                            14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                     12-DEC-1997;
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                                                                                                                                                                                                                                     WO9931132-A1
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AAY23737;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Nhha surface antigen polypeptides and polynucleotides from Neisserla meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                 Surface antigen NhhA; meningococcal disease; meningitis vaccine; mutant; mutein.
                                                                                                                                                                     /label- Signal_peptide
52.513
Alabel- Mature_NhhA_deletion_mutant
/note="predicted mature protein, specifically
claimed in claim 12"
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         N. meningitidis H41 NhhA deletion mutant.
                                                                                                                                     Location/Qualifiers
                                                                                    Neisseria meningitidis strain H41.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 6; 91pp; English.
                                                                                                                                                                                                                                                                                                                                  25-JAN-2001; 2001WO-AU00069.
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N-PSDB; AAS09173.
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
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APPLICANT: PEAK, Ian Richael Paul
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 05604/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: CT/ANU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1989-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 11, Application US/09377155 ; Patent No. 6197312
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; Sequence 21, Application US/09377155
; Patent No. 6197312
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                                                                                                                       27.1%; Score 161; DB 4; Length 591; 100.0%; Pred. No. 3.3e-144; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.3e-144;
tive 0; Mismatches 0;
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GENEKAL INFORMATION:
GENEKAL INFORMATION:
GENEKAL INFORMATION:
GENEKAL GENEK, MICHAEL PAUL
APPLICANT: JENNINGS, MICHAEL PAUL
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REPERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR PILING DATE: 1999-08-19
PRIOR PILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-12
SPRIOR FILING DATE: 1999-12-12
NUMBER: OF SEQ ID NOS: 33
SOFTWARE: PALENTIN VET: 2.0
SEQ ID NO 11
LENGTH: 591
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; Sequence 21, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
                                 ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21
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                                                                                                                                         Best Local Similarity 100.
Matches 161; Conservative
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; SEQ ID NO 21
; LENGTH: 591
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100.0%; Pred. No. 3.3e-144;
Live 0; Mismatches 0; Indels
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENINGS, Michael Paul
APPLICANT: JENINGS, Michael Paul
APPLICANT: JENINGS, MICHAEL
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT APPLICATION NUMBER: US/09/377,155
FRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATCHIN VOR: 2.0
APPLICANT: JENNINGS, Michael Faul
APPLICANT: MOXON, E. Richard
FILLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 06504/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: DCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR PLING DATE: 1999-12-14
PRIOR PLING DATE: 1997-11-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATCHIN VEY: 2.0
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; Sequence 2, Application US/09377155
; Patent No. 6197312
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US-09-377-155-2
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374 YDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT 433
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DENK, Ian Richard Anselm
APPLICANT: WOXON, E. Richard
TITLE OF INVEWTION.
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: US/09/669,974
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
SEQ ID NORES: BALCHARD NORMER: GE SEQ ID NORES: 33
SOFFWARE: PATCHIL VOYE: 2.0
SEQ ID NO 19 PATCHIL OF THE NORE: SEQ ID NOS: 33
LEWSTH. 589
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Patent No. 6197312
SERERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-669-974-19; Sequence 19, Application US/09669974; Patent No. 6333173
; ORGANISM: Neisseria meningitidis
US-09-377-155-19
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Best Local Similarity
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US-09-377-155-17
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365 DQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIN 424
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Best Local Similarity 100.0%; Pred. No. 3.3e-144;
Matches 161; Conservative 0; Mismatches 0; Indels
                                                                          426 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 466
                                                                                                              425 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 465
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APPLICANT: PEAK, Tan Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENY FILING DATE: 1999-08-19
PRIOR RILING DATE: 1999-114
PRIOR PELLICATION NUMBER: PCT/AU98/01031
PRIOR PELLICATION NUMBER: CG 9726398.2
PRIOR FILING DATE: 1999-12-14
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APPLICANT: PEAK, IAN RICHARD ANSELM:
APPLICANT: PEAK, IAN RICHARD
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON. E. RICHARD
FILE REPERBONE: 06504/0128
CURRENT APPLICATION NUMBER: US,09/669,974
CURRENT PILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-12
PRIOR PREDICATION NUMBER: GB 9726398.2
PRIOR PREDICATION NUMBER: GB 9726398.2
PRIOR PREDICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1999-12-12
SROFTWARE: PATENTING DATE: 1997-12-12
SROFTWARE: PATENTING PATE: 1997-12-12
SROFTWARE: PATENTING PATE: 1997-12-12
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SROFTWARE: PATENTING PATE: 1997-12-12
SROFTWARE: PATENTIN VET: 2.0
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                                                                                                                                                                                                                                                                       Sequence 2, Application US/09669974; Patent No. 6333173; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2
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SOFTWARE: Pat
SEQ ID NO 19
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US-09-669-974-2
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494 GDVTNVAQLKGVAQNLNN 511
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US-09-377-155-13
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Best Local Similarity 100.0%; Pred. No. 2e-122;
Matches 138; Conservative 0; Mismatches 0; Indels
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2e-122;
hes 0;
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       CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
SOFTWARE: PATENTIN OFF: 130
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APPLICANT: PEAK, IAN RICHARD ANSEL
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
ITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1999-12-12
O65064/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/09669974 Patent No. 6333173
                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-17
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 592
TITLE OF INVENTION:
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100.0%; Pred. No. 2e-122;
ative 0; Mismatches 0
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
SPELOR STREAM ON E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-14
PRIOR FILING DATE: 1997-12-14
SPRIOR FILING DATE: 1997-12-12
NUMBER OF SEO ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DEMK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE FEFENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
SOFTWARE: PALCHIN VET. 2.0
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; Patent No. 6197312
                                                                                                                     US-09-377-155-5; Sequence 5, Application US/09377155; Patent No. 6197312
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Best Local Similarity 100.0%; Pred. No. 2e-122; Matches 138; Conservative 0; Mismatches 0; Indels
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GEMERAL INCHMATION
APPLICANT: PEAK, IAI RICHAED RAUI
APPLICANT: DENNINGS, Michael Paul
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richaed
TITLE GENERALE: 050504/0128
FTILE REFERENCE: 050504/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: US/09/77,155
PRIOR PILLING DATE: 1999-08-19
PRIOR RAPLICATION NUMBER: GB 9726398.2
PRIOR RILING DATE: 1998-12-14
PRIOR PILLING DATE: 1999-12-12
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 5
LENGTH: 598
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US-00-669-974-5
Sequence 5, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
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; ORGANISM: Neisseria meningitidis
US-09-669-974-5
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Search completed: September 5, 2002, 10:41:15 Job time: 261 sec

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AGNNIEI 430
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Matches 161;
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R. Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A. Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUID:20175755
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-591 <- Text-A;
A; Cross-references: GB:AE002450; GB:AE002098; NID:97226229; PIDN:AAF41395.1; PID:9722623
A; Experimental source: serogroup B, strain MC58
C; Genetics:
A; Gene: NMB0992
                                                                                                                5, 2002, 10:38:14 ; Search time 33.9 Seconds (without alignments) 1683.689 Million cell updates/sec
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probable surface f
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C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                  283138 seqs, 96089334 residues
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    protein search, using sw model

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length: 2000000000
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C;Accession: A81888
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mc; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
A;Reference number: A81775; MUID:20222556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-592 <PAR>
A;Residues: 1-592 <PAR>
A;Cross-references: GB:ALL62755; GB:AL157959; NID:g7379742; PIDN:CABB4461.1; PID:g737
A;Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
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100.0%; Pred. No. 5e-121;
tive 0; Mismatches 0; Indels
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h 27.1%; Score 161; DB 2; Le Similarity 100.0%; Pred. No. 8.7e-156; 61; Conservative 0; Mismatches 0;
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5, 2002, 10:41:54

Thu Sep 5 14:35:54 2002

**-**}

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

September 5, 2002, 10:41:19 ; Search time 19.15 Seconds
(without alignments)
1201.014 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-700-293-2 594 1 MNKIYRIIWNSALNAWVAVS.....TASGNSRGHFGASASVGYQW 594

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

105224 seqs, 38719550 residues Searched:

20 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen, parameters:

Post-processing: Listing first 1000 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Query Score Match Length DB No. Score Match Leng Result

Search completed: September 5, 2002, 10:48:19 Job time: 420 sec

No matches found

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9

neisseria m neisseria m neisseria m neisseria m neisseria m neisseria m nemophilus haemophilus

091928 091981 091981 091917 091919 091986 048152

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STRAIN-EG327;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF157605; AAK68866.1; -
SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3A8EA2 CRC64;
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01-DEC-2001 (TrEMBLrel.
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Bacteria; Proteobacter:
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SEQUENCE FROM N.A.
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374 YDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT 433
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     Neisseria meningitidis.
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TAXID=487;
                                                                                                                                        MEDLINE=2017556; Pubmed=10710308;

MEDLINE=20175756; Pubmed=10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldil L., Bartolini E., Capecchi B., Galectti C.L., Luzzi E., Manetti E., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.W., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B Meningococus by Whole-Genome Sequencing";

EMBL; AF226379; AAF42811; C., SEQUENCE 594 AA; 62114 MW; IE2A63A78F53D256 CRC64;
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MEDIJINE=201, AND 1000;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Galectti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Ratti G., Santini E., Rappe B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

Mentification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole Genome Sequencing.";
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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EMBL; AF226356; AAF42505.1;
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RC STRAIN-NG3/88, AND BZ232;

RX MEDLINE-2017516; Pubmed=10710308;

RA MEDLINE-2017516; Pubmed=10710308;

RA COMMANDELS N. MASSIGNANI V., Giuliani M.M., Arico' B.,

RA Pizza M., Scarlato V., Masgignani V., Giuliani M.M., Arico' B.,

RA Galecti C.L., Luzzi E., Manetti R., Marchetii E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Moxon E.R., Grandi G., Rappuoli R.; Mason T., Tettelin H.,

RA Moxon E.R., Grandi G., Rappuoli R.; Mason T., Tettelin H.,

RA Moxon E.R., Grandi G., Rappuoli R.; Mason T., Tettelin H.,

RA Moxon E.R., Grandi G., Rappuoli R.; Serogroup B

RT Science 287:1816-1820(2000).

BR EMBL; AF226376; AAR42555.1; -

CTANIRNCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;
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Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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MEDLINE-20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
I'dentification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
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  Length 595;
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100.0%; Pred. No. 3e-147;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF226361; AAF42510.1; -.
SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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                                                                                                                                                                                     554 EAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
37.2%; Score 221; DB 2; L. 100.0%; Pred. No. 4e-204; Live 0; Mismatches 0;
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01-OCT-2000 (TrEMBLrel. 15, Created)
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           Local Similarity 100. ies 221; Conservative
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Best Local Similarity 100.
Matches 162; Conservative
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 Query Match
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Matches
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306 GEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKD 365
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.3%; Score 162; DB 2; Length 598; 100.0%; Pred. No. 3e-147; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF226385; AAF42534.1; -.
SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0UTER MEMBRANE PROTEIN GNA992.
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MEDLINE=20175756; PubMed=10710308;
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MEDLINE=20175756; PubMed=10710308;
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SEQUENCE FROM N.A.
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Length 599;

DB 2;

Score 162;

27.3%;

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Gaps 0;

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SEQUENCE FROM N.A.
STRAIN-MICS A SERGGROUP B;
STRAIN-MICS B A SERGGROUP B;
MEDLINE-20175755; PubMed-10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parkey D.S., Blair E., Cittone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scaltaco V., Masignani V., Pizza M., Grandi G., Sun L.,
Sanith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
"Complete genome sequence of Neisseria meningitidis serogroup B strain
MCC58";
                                                SEQUENCE FROM N.A.
STRAIN=EG329;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Subnitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ART6560; ARK68867.1; - CDC600798859C65 CRC64;
SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;
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Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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MEDLINE_20175756; PubMed=10710308;
Pizza M. Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Pizza M. Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Pizza M. Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Galeotti C. L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Ratti G., Santini E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
Moxon E.R., Grandi G., Rappuoli R.;
Mentification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
  Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TTEMBLE). 15, Last sequence update)
01-DEC-2001 (TTEMBLE). 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE
                                                                                                                                                                                                                            Query Match 27.1%; Score 161; DB 2; Length 591; Best Local Similarity 100.0%; Pred. No. 2.7e-16. Matches 161; Conservative 0; Mismatches 0; Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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NCBL_TaxID-487;
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                  Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NHA OUTER MEMBRANE PROTEIN.
NHHA.
                                                                                                                                                                                                          431 AGNNIEITERNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDD 472
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCT-2001 (TrEMBLrel. 19, Last annotation update)
0UTER MEMBRANE PROTEIN GNA992.
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100.0%; Pred. No. 3e-147;
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us-09-700-293-2.oligo20.rspt

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SEQUENCE FROM N.A.
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                                                        Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer membrane protein of Netsseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226375; AAF42524.1;
EMBL; AF226577; AAF42516.1;
EMBL; AF226577; AAF42519.1;
EMBL; AF226577; AAF42519.1;
EMBL; AF226374; AAF42519.1;
EMBL; AF226374; AAF42519.1;
EMBL; AF226374; AAF42519.1;
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
"Identification and characterisation of a gene encoding a novel outer
membrane protein of Naisseria meningitidis.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125375; AAK09943.1;
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592 AA; 62290 MW; 168986A97381EFC5 CRC64;
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100.0%; Pred. No. 2.7e-146;
ive 0; Mismatches 0;
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                   SEQUENCE FROM N.A. SPECIES=N.meningitidis; STRAIN=PMC21;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
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0UTER MEMBRANE PROTEIN.
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Q9AQF0
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374 YDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIT 433
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF157610; AAK68871.1; -
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"Identification of Vaccine Candidates Against Serogroup B Meningococus by Whole-Genome Sequencing.";
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EMBL; AF226362; AAF42511.1; -.
EMBL; AF226363; AAF42512.1; -.
SEQUENCE 589 AA; 61520 WW; 2B2A95D4868566A6 CRC64;
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589 AA; 61448 MW; 1F1A80CD610CB230 CRC64;
                                                           (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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589
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STRAIN-NGP165, 90/18311, AND 93/4286;
MEDLINE-20175756; Pubmed-10710308;
PRT;
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Matches 138; Conservative
PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIM-NGE28;
MEDLINE-2017576; PubMed-10710308;
MEDLINE-2017576; PubMed-10710308;
MEDLINE-2017576; PubMed-10710308;
MEDLINE-2017576; PubMed-10710308;
MEDLINE-2017576; PubMed-10710308;
MEDLINE-2017576; PubMed-10710308;
MEDLINE-201756; PubMed-10710308;
MEDLINE-20176; PubMed-10710308;
MEDLINE-20176;
MEDLINE-20176; PubMed-10710308;
MEDLINE-20176; PubMed-1071030
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Query Match 23.2%; Score 138; DB 2; Length 569
Best Local Similarity 100.0%; Pred. No. 46-124,
Matches 138; Conservative 0; Mismatches 0; Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NHHA OUTER MEMBRANE PROTEIN.
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                  Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                  NCBI_TaxID=487;
                                     Bacteria;
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A surface protein
N. meningitidis P4
A surface protein
N. meningitidis P2
N. meningitidis P2
N. meningitidis P2
N. meningitidis P3
N. meningitidis P4
Amino acid sequenc
N. meningitidis P4
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N. meningitidis P4

influe influe

Haemophilus Haemophilus Neisserial

Haemophilus influe

M. catarrhalis les Escherichia coli p Moraxella catarrha

New protein and its nucleotide sequence, useful in vaccines or diagnostic compositions for treating and/or preventing Neisseria  $\,$ 

WPI; 1999-444400/37 N-PSDB; AAX99124.

26439

Result

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Scarlato

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protein; pharmaceutical; vaccine; diagnosis;
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AAR99394
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AAB23858
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bacterial infection; treatment
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09-OCT-1998;
14-JAN-1998;
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BASB029 amino acid
N. meningitidis EG
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                                                                                                                                                                                                                                                           .....TASGNSRGHFGASASVGYQW 591
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                  4.5
Compugen Ltd
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                GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
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Listing first 45 summaries
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AAY23741
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AAU6174

    protein search, using sw model

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AAU06171
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Neisseria meningitidis
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                                                    The invention provides proteins (AAY27201-245) from Neisseria menigitidis (strains A and B) and nucleic acid sequences (AAX99123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition are dagnostic composition. The composition is also useful for treating or preventing an infection due to Neisserial bacteria, especially Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                          61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
                                                                                                                                                                                                                                                                                                                                                                                  NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 360
                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                          0
                                                                                                                                                                                                           99.9%; Score 2999; DB 20; Length 591; 99.8%; Pred. No. 1.9e-171; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A surface protein of Neisseria meningitidis.
                             Claim 1; Page 62; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY23746 standard; Protein; 591
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                                                                                                                                                                                                                           Best_Local Similarity 99.8
Matches 590; Conservative
meningitidis infections
                                                                                                                                                                   591 AA;
                                                                                                                                                                       Sequence
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NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a surface protein of Neiserria menigitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans. The N. meningitidis infection in humans. The N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
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                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis surface proteins useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 127-128; 132pp; English.
                                                                                                                                                                                                                                             Peak IRA;
                                                  98WO-AU01031.
                                                                                                       97GB-0026398.
                                                                                                                                                            (ISIS-) ISIS INNOVATION LTD. (UYQU ) UNIV QUEENSLAND.
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                                                                                                                                                                                                                                             Moxon ER,
                                                                                                                                                                                                                                                                                                                                                                                                       meningitidis infections
                                                                                                                                                                                                                                                                                            WPI; 1999-418754/35.
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24-JUN-1999
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590;
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Best Local Si
Matches 590;
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                     Claim
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AC AAY5
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Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                         N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                        /note= "Predicted mature protein, specifically
claimed in claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New NhhA surface antigen polypeptides and polynucleotides from
                          MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                   1..50
/label= Cl
/note= "Conserved region 1"
                                                                                                                                                                                                                                                                                                                                                         237..591
/label= C5
/note= "Conserved region 5"
                                                                                                                                                                                                                                                  'note= "Conserved region 2"
                                                                                                                                                                                                                                                                                         "Conserved region 3"
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                                                                                                                                                                                                                                                                                                                          /label= C4
/note= "Conserved region
                                                                                                                                                                                            /label= V1
/note= "Variable region
                                                                                                                                                                                                                                                                     /note= "Variable region
                                                                                                                                                                                                                                                                                                      /label= v3
/note= "Variable region
                                                                                                                                                                                                                                                                                                                                             /label= V4
/note= "Variable region
                                                                                                                                                      1..51
/label= Signal_peptide
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                 /label= Mature_NhhA
                                                                                                                                  meningitidis strain PMC21
                                                                 Ā
                                                                 AAU06171 standard; Protein; 591
                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001; 2001WO-AU00069
                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2000; 2000US-0177917
                                                                                                                                                                                                                                            /label- C2
                                                                                                                                                                                                                                                                /label= V2
                                                                                                                                                                                                                                                                                  /label= C3
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                210
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                                                                                                                                                                                                                                                         .124
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                                                                                                                                                                                                                                                                                          'note=
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N-PSDB; AAS09161.
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                                                                                           24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-2001
                                                                                                                                   Neisseria
                                                                              AAU06171;
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The present invention relates to the isolation of novel Neisserla meningitidis mutant polypeptides of the surface antigen Nhh AAU061865. The modified or mutant Nhhh polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain 10 10 Nhh polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
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     or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
Neisseria meningitidis, useful in producing vaccines preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2999; DB 22; Pred. No. 1.9e-171;
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                                                                          Fig 1; 91pp; English.
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99.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention.
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This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain #44/76. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HEF) protein. The invention relates to BASB029 polymuclectide sequences (AAZ39864-Z39865) and polypeptide sequences (AAZ39864-Z39865) and polypeptides are useful in a menmal. Compositions containing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polypeptides and polypeptides are useful for generating an autibody objunclectides and polypeptides are useful for generating an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polymuclectide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the particularly genetic immunisation. Antibodies against BASB029 polymuclectides and for therapeutic or prophylactic purposes, polymuclectides and for therapeutic or prophylactic purposes, polymuclectides and dortherapeutic or prophylactic purposes, polymuclectides and dortherapeutic naminosation. Antibodies against BASB029 polymuclectides and doubpeptides are also useful for treating infections particularly genetic immunisation. Antibodies against BASB029 polymuclectides and doubpeptides are also useful for treating in the protein is useful for the stimulation of the immune system of an organism processiving the protein and development of antibacterial drugs. Fused recombinant
                                                                                        BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
                                                       BASB029 amino acid sequence from N. meningitidis strain H44/76.
                                                                                                                                                                                                                                                                                                                                            /note= "Encoded by AATC"
                                                                                                                                                                                                                                                                                                                                                                /note= "Encoded by ACA"
Misc-difference 269
                                                                                                                                                                                                                                               /note= "Encoded by GAT"
Misc-difference 98
                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Encoded by AAA"
389
                                                                                                                                                                                                                                                                                                    'note= "Encoded by AAC"
                                                                                                                                                                                                                         'note= "Encoded by AAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Encoded by CGT"
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                                                                                                                                                                                        Location/Qualifiers
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               21-FEB-2000 (first entry)
                                                                                                                                                  Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                          Misc-difference 108
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Misc-difference 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAY-1998;
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61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
                                                   121 NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
                                                                                          GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF 240
                                                                                                                                                              241 VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS 300
                                                                                                                                                                                                                                             SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV 420
                                                                                                                                                                                                                                                        421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 480
                                                                                                                                                                                                                                                                                                                             481 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM 540
           1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                                                                                                                                                                                                                                                                                                                                                   541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                                                                                               Surface protein; surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A surface protein of Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoreactive peptide.
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N-PSDB; AAX85793.
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Gaps

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Length 591; Indels

99.3%; Score 2981; DB 21; 99.2%; Pred. No. 2.3e-170; iive 5; Mismatches 0;

Query Match Best Local Similarity 99.2 Matches 586; Conservative

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Surface antigen NhhA; meningococcal disease; meningitis vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                   ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM 540
                                                                                                                                                                                                                    YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
                                                                                                                                                                                                                             NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 480
                                                                                                                                                                    Gaps
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                                                                                                                                                                                            1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                                                                                                                                                                                                                                                                                                                                         TDEGEGLVTAKEVIDAVNKAGWRMFTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                                                                                                                                                                                                                                      GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                                                                                                                                        VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                          humans
                                        The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N. meningitidis EG329 surface antigen NhhA polypeptide sequence.
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Neisseria meningitidis surface proteins useful for treating N.
                                                                                                                                                    Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                    Indels
                                                                                                                                                  Score 2980; DB 20;
Pred. No. 2.6e-170;
1; Mismatches 3;
                        Claim 1; Page 104-106; 132pp; English
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                                                                                                                                                   99.28;
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                                                                                                                                                  Query Match 99.2
Best Local Similarity 99.3
Matches 587; Conservative
        meningitidis infections
                                                                                                                           591 AA;
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                                                                                                                           Sequence
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AMU06182-AMU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain EG329 is 1 of 10 NhhA polypeptide sequences (AAU060771-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or
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/label= Cl
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/label= C4
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/label= C5
/note= "Conserved region
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/note= "Variable region
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Neisseria meningitidis strain EG329
                                              Location/Qualifiers
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/note= "Conserved
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/label= V4
/note= "Variable
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                                                                                                                                                                                                                                                                                                                                                                                                                      189..210
/label= v3
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N-PSDB; AAS09165.
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99.2%; Score 2980; DB 22; Length 591;

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                                                                                                  VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS 300
                                                                                                                                                                  61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
                                                                                                                                                                                         TDEGEGLUTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 360
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                                                                                                                                                                                                                                                         NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 480
        0; Gaps
                                 1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60
                                                                                                                                                                                                                                                                                         481 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                                                                                                                                                                                                                                        541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                                                 Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.
         Indels
99.3%; Pred. No. 2.6e-170; ive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                  surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                 AAY23737 standard; Protein; 592 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jennings MP, Moxon ER, Peak IRA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS INNOVATION LTD. (UYQU ) UNIV QUEENSLAND.
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
Best Local Similarity 99.39
Matches 587; Conservative
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60 LYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 NGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGS 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                              The present sequence represents a surface protein of Neiserria menigitidis which is approximately 62 KDs. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis auffection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis surface proteins useful for treating meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                             98.8%; Score 2967.5; DB 20; Length 98.8%; Pred. No. 1.4e-169; tive 3; Mismatches 3; Indels
                                                                  Claim 1; Page 86-87; 132pp; English
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Matches 585; Conservative
                                                                                                                                                                                                                                                                                                                                                             592 AA;
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Best Local S
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WPI; 2000-053103/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         meningitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a surface protein of Neiserria
                                                                                                                                                                                                                                                                                    meningitidis surface proteins useful for treating
                        surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.0%; Score 2762.5; DB 292.5%; Pred. No. 2.6e-157; Ive 14; Mismatches 20;
A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                       Claim 1; Page 100-101; 132pp; English.
                                                                                                                                                                                                                        Peak IRA;
                                                                                                                                    98WO-AU01031.
                                                                                                                                                                                  INNOVATION LTD.
QUEENSLAND.
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Best Local Similarity 92.5
Matches 553; Conservative
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                                                                                                                                                                                                                      Jennings MP, Moxon ER,
                                                            Neisseria meningitidis.
                                    immunoreactive peptide
                                                                                                                                                                                                                                               WPI; 1999-418754/35.
N-PSDB; AAX85792.
                         protein;
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                                                                                   W09931132-A1.
                                                                                                                                                             12-DEC-1997;
                                                                                                                                    14-DEC-1998;
                                                                                                          24-JUN-1999
                                                                                                                                                                                                                                                                                    Neisseria
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                         Surface
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This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain ATCC13090. The BASB029 protein is homologous to the serogroup B strain ATCC13090. The BASB029 protein is homologous to the memophilus influenzes surface fibril (HSF) protein. The invention relates to BASB029 polypucleotide sequences (AAX57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polypucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polypucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polypucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the combinant correction is useful for the stimulation of the immune system of an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.
                     KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSK 473
                                                                             474 KDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA 533
                                                                                                                                                                                BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
                                                                                                                                                         534 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                                                                                                                                                                                                                                                                                                                                                                        TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 354
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                                                        Query Match
92.0%; Score 2762.5; DB 21; Length 594;
Best Local Similarity 92.5%; Pred. No. 2.66-157;
Matches 553; Conservative 14; Mismatches 20; Indels 11; Gaps
                                                                                                                                               1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60
                                                                                                                                                                       534 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
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/note= "Conserved region 1"
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594 AA;
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strains than meningitidis strains than the N. meningitidis strains given in AMAU06180) from 10 different N. meningitidis strains given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New NhhA surface antigen polypeptides and polynucleotides from beisseria meningitudis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
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                                                                                                   /label= C3
/note= "Conserved region 3"
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/note= "Conserved region 5"
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/note= "Variable region 4"
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/label= V2
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N-PSDB; AAS09164.
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be used to identify immunoreactive peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kps. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerse, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, is the form of vaccines. The proteins and antibodies can also
                                       TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWN1KGVKPGTTA
        SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDK
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                                                                                                                                                                                                                                                                                                                         Surface protein; surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                         protein of Neisseria meningitidis.
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                                                                            11;
                                              Length 594;
                                          ; Score 2736.5; DB 20; Lengt; Pred. No. 9.4e-156; 11; Mismatches 26; Indels
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/label= V1
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92.0%;
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Matches 550;
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ntnentndssftyslkkdltdltsveteklsfgangnkvnitsdtkglnfaketagtngd 176
                                                                                                                   SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDK 294
                                                                                                                                          295 GENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 354
                                                                                                                                                                                                                                                                                                                                                      415 KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSK 473
                                                                                                                                                                                                                                                                                                                                                                               474 KDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kbs. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally at thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to
                                           175 TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis surface proteins useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Surface protein; surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 108-110; 132pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of novel Neisseria meniggitidis mutant polypoptides of the surface antigon Nhha (AAU06188). The modified or mutant Nhha polypoptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis, and in designing madicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhh from N. meningitidis strain BZ198 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.1%; Score 2736.5; DB 22; Length 594;
Best Local Similarity 92.0%; Pred. No. 9.4e-156;
Matches 550; Conservative 11; Mismatches 26; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NbhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producting vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
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/note= "Conserved region 5"
"Conserved region 2"
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/note= "Variable region 3"
                                                        "Variable region 2"
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239..59
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    /note=
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"Conserved region 1"

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                                                                                                                      61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
                                                                                                                                            -----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG 170
                                                                                                                                                                        TNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 230
                                                                                                                                                                               GKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF 350
                                                                                                                                                                                                                                                               351 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS 410
                                                                                                                                                                                                                                                                                            PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALN 469
                                                                                                                                                                                                     GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVT 290
                                                                   Gaps
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                                                                                1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60
                                                                                                                                                                                                                                                                                                                                  VGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                                                                                                                                                                                                                                                                                                                                              530 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY
prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease; meningitis vaccine.
                                                    DB 20; Length 598;
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                                                                  28; Indels
                                                   90.6%; Score 2721.5; DB 20
90.9%; Pred. No. 7.5e-155;
ive 12; Mismatches 28;
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/label= C1
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ses 547; Conserv
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh (AMU06182-AANU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain H15 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
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90.9%; Pred. No. 7.5e-155;
ive 12; Mismatches 28;
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/note= "Conserved region
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/label= V1
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/note= "Variable
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N-PSDB; AAS09167.
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Claim 1; Page 91-93; 132pp; English.
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        -----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG 170
                                        171 TNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 230
                                                                      GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVT 290
                                                                                                    GKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF 350
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                                                                                                                                                                                                                      VGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 529
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gw 598
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121 -----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a surface protein of Neiserria menigitidis which is approximately 62 Kpa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans. The torn of vaccines. The proteins and antibodies can also be used to lot the form of vaccines. The proteins and antibodies can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALN
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90.3%; Score 2712.5; DB 20; Length 598;
Best Local Similarity 90.5%; Pred No. 2.6e-134;
Matches 545; Conservative 13; Mismatches 29; Indels 15;
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Job time: 478 sec
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Query Match 99.9
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Pred. No. 6.7e-225;
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Sequence_21_Application US/09377155
Sequence_21_Application US/09377155
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: MOXON, E. Richard
I TILLE OF INVENTION: NOVEL SUFFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILING DATE: 1999-08-19
PRIOR PILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
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NUMBER OF SEO IN NO. NO.
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US-09-377-155-21
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Matches 587; Conservative
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US-09-377-155-11
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99.9%; Score 2999; DB 4; Length 591;
Best Local Similarity 99.8%; Pred No. 6.7e-225;
Matches 590; Conservative 0; Mismatches 1, Indels 0
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APPLICANT: PEAK, IAN RICHARD ANSELM
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. RICHARD
TITLE OF INVENITON: NOVEL, SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
FILE REFERENCE: 065064/0129
FURRENT FILING DATE: 000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR PILING DATE: 1999-08-19
PRIOR PELING DATE: 1998-11-14
PRIOR PELING DATE: 1998-12-14
PRIOR PELING DATE: 1998-12-14
PRIOR PELING DATE: 1997-12-12
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US-09-669-974-21
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301 TDEGEGLUTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 360
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APPLICANT: PERK, Ian Richael Paul
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 0550440128
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1988-12-14
PRIOR FILING DATE: 1988-12-14
PRIOR FILING DATE: 1989-12-12
PRIOR FILING DATE: 1989-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6197312
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US-09_377-155-11
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420 VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 479
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Best Local Similarity 99.3%; Pred. No. 2e-223;
Matches 587; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                 APPLICANT: PEAK, Tan Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard File OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1997-12-14
SOFTWARE: PARIOR DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENT VET. 2.0
SSOTUND 11
LENGTH: 591
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Patent No. 66331737
GENERAL INFORMATION:
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ORGANISM: Neisseria meningitidis
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                                                                   NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
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Pred. No. 1.9e-222;
3; Mismatches 3;
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: U5/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
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98.8%;
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Matches 585; Conservative
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SOFTWARE: PatentIn Ve
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KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK 476
421 VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV 480
                                      480 RITHVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDK 294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%; Score 2762.5; DB 4; Length 594;
92.5%; Pred. No. 1.6e-206;
Live 14; Mismatches 20; Indels 11; Gaps
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                                                                                                                                    540 MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                                                                      APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: ROVEL SURFACE ANTIGEN
FILE REPERBNCE: 065064/0128 (SOF)
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/4098/01031
PRIOR PFLING DATE: 1999-12-14
PRIOR PLING DATE: 1999-12-14
PRIOR PLING DATE: 1999-12-14
                                                                                                                                                                                                                          MS-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Neisseria meningitidis US-09-377-155-9
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 92.0%
Best Local Similarity 92.5%
Matches 553; Conservative
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LENGTH: 594
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                                                        RITHVAPGVKEGDVTHVAQLKGVAQNLHNRIDHVDGNARAGIAQAIATAGLVQAYLPGKS 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGIGSTLTDTLLINTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVD 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.8%; Score 2967.5; DB 4; Length 592; 98.8%; Pred. No. 1.9e-222; tive 3; Mismatches 3; Indels 1;
                                                                                                                                  540 MMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                      APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS. Michael Paul
APPLICANT: JENNINGS. Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REPERENCE: 055064/0128
CURRENT APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1997-12-14
PRIOR FILING DATE: 1997-12-14
SEQ ID NOS: 33
SOFTWARE: PATENTIN VOYER: 20
                                                                                                                                                                                                                                                                     Sequence 2, Application US/09669974; Patent No. 6333173
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US-09-669-974-2
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US-09-669-974-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
                                                                                                                                                                                                    APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR PLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
                                                                                                                                                    Sequence 7, Application US/09377155 Patent No. 6197312
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61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
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                                                                    YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
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92.5%; Pred. No. 1.6e-206;
ive 14; Mismatches 20;
                                                                                                                                                                                                   APPLICANT: PEAK, IAN RICHARD ANSELM
APPLICANT: PEAK, IAN RICHARD ANSELM
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR PILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
PRIOR FILING DATE: 1999-12-12
                                                                                                                                                                      Sequence 9, Application US/09669974 Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Neisseria meningitidis US-09-669-974-9
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SOFTWARE: PatentIn Ver. 2.0
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es 553; Conserv
                                                                                                                                  RESULT 8
US-09-669-974-9
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237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK 296 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDK 294 GENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 354 GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 414 415 KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSK 473 KDNKPVRITHVVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA 533 61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120 Gaps 57 1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60 1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLFFATVQANATD---DDDL 11; Length 594;

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121 -----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG 170
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                                                                                                                                                       APPLICANT: DENNINGS, Michael Paul
APPLICANT: DENNINGS, Michael Paul
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064 /0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALENT: 1997-12-12
NUMBER OF SEQ ID NOS: 33
LENGTH: 598
                                                                                                ; Sequence 13, Application US/09377155; Patent No. 6197312; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.6%
Best Local Similarity 90.9%
Matches 547; Conservative
                                                           RESULT 11
US-09-377-155-13
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                                                                                                                                                                        APPLICANT: DEAK, Ian Richard Anselm, APPLICANT: DENNIGS, Michael Paul, APPLICANT: JENNIGS, Michael Paul, APPLICANT: JENNIGS, Michael Paul, APPLICANT: JENNIGS, Michael Paul, TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFRENCE: 05604/0128
CURRENT APPLICATION NUMBER: US,09/377,155
PRIOR APPLICATION NUMBER: US,09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-114
PRIOR FILING DATE: 1999-12-14
SPRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                     ; Sequence 7, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Neisseria meningitidis
US-09-669-974-7
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Matches 550; Conservative
                                                                              SULT 10
-09-669-974-7
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61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
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537 LAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGY 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TILE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: CT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Mismatches
                                                                                                           US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
COGANISM: Neisseria meningitidis
US-09-377-155-5
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90.5%;
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Matches 545; Conservative
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SOFTWARE: PatentIn Ve
                                                                                                                                                       GENERAL INFORMATION:
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QW 598
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; Pred. No. 2.4e-203;
12; Mismatches 28;
                                                               US-09-669-974-13
Sequence 13, Application US/09669974
Patent No. 6333173; GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm; APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN; FILE REFERENCE: 065064/0128
                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR PELLING DATE: 1000-09-26
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATCHIN VET: 2.0
SOFTWARE: PATCHIN VET: 2.0
SOFTWARE: 98
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Best Local Similarity 90.9%
Matches 547; Conservative
             598
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Gaps

57

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530 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY 589
                                                               477 VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 536
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                                                                                                                                                                                                                                                                                                        APPLICANT: DERAY, IAN Richard Anselm
APPLICANT: DENANGS, Michael Paul
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION. E. Richard
FILE REFERENCE: 06506/4012
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                        ; Sequence 15, Application US/09377155 ; Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15
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                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                   590 QW 591
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121 ------NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG 170
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                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: PEAK, IAI Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON. E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILER REFERENCE: 065064/0128
CURRENT PILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-12
PRIOR FILING DATE: 1999-12-12
PRIOR FILING DATE: 1999-12-12
SRIOR FILING DATE: 1999-12-12
SRIOR FILING DATE: 1999-12-12
SRIOR FILING DATE: 1999-12-12
SROFTWARE: PATENTIN NUMBER: GB 9726398.2
SOFTWARE: PATENTIN VOR: 3.0
                                                                                                                                                     RESULT 14
US-09-669-974-5
Sequence 5, Application US/09669974
Patent No. 6333173
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Neisseria meningitidis
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Best Local Similarity 90.55
Matches 545; Conservative
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                                                        590 QW 591
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; Search time 34.15 Seconds (without alignments)
1662.922 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 MNKIYRIIWNSALNAWVAVS.
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Maximum Match 100%
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length: 2000000000
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                                                                                                    September
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Sequence:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

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Gaps

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Length 591; Indels 9

g δy g

MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL

/ Match 99.9%; Score 2999; DB 2; Local Similarity 99.8%; Pred. No. 1.3e-140; les 590; Conservative 0; Mismatches 1;

Query Match Best Local S: Matches 590,

A;Gene: NMB0992

181 241

GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF

TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 

VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS

NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN

121 121 181

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300 300 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV 420

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surface protein XF probable adhesin Z probable adhesin E probable surface p surface-exposed ou hypothetical prote high-molecular-wei ABC-type transport probable adhesin h hypothetical prote hypothetical prote adhesin NMB0992 [i probable surface f adhesin homolog HI surface protein XF probable autotrans adhesin AIDA-î pre AidA-I adhesin-lik probable adhesin Z surface-array prot ydeK protein - Esc hemagglutinin/hemo sapB protein - Cam probable adhesin P hemolysin A precur filamentous hemagg probable RTX famil hemolysin (importe Description SUMMARIES G81133 A81888 I64138 D82671 AC0976 A82615 A86036 H91188 AH0110 C82672 G64964 A43855 B43399 AF0394 AF0394 F90696 В Query Match Length Score 

30	200.5	6.7	1343	20	D85724	hypothetical prote
32	198.5	9.0	1487	4 (	AG2560	hypothetical prote
33	197.5	9.9	1343	2	E90893	
34	197	9.9	585	~	F90961	⋿
35	197	9.9	585	~1	F85809	hypothetical prote
36	195	6.5	1461	~	A85547	
37	194.5	6.5	1428	7	AC2224	hypothetical prote
38	194.5	6.5	3029	7	S76109	hypothetical prote
39	194	6.5	3705	7	AD0123	probable autotrans
40	193.5	6.4	3013	~	AB0480	probable invasin Y
41	193.5	6.4	4936	7	AH2515	hypothetical prote
42	192	6.4	1430	~	AF0351	probable autotrans
43	191.5	6.4	1335	7	T17508	glycoprotein Vp260
44	191.5	6.4	1608	7	A28182	hemolysin A - Serr
45	191	6.4	2249	7	A41477	190K surface antig
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RESULT	1					
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adhesin	adhesin NMB0992 [imported] - Neis C.Species: Neisseria meningitidis	(import	- 5	Nei	sseria mening	- Neisseria meningitidis (strain MC58 serogroup B)
C; Date:	C; Date: 31-Mar-2000	000 #SE	edneuce	re	vision 31-Mar	#sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C; Acces:	C; Accession: G81133	133				
R; Tette	lin, H.;	Saunder	rs, N.	·	Heidelberg, J	Jeffries, A.C.; Nelson, K.E.; Eisen
Hickey,		It, D.I Vamatł	H.; Sal	ZDE	Hickey, E.K.; Hait, D.H.; Salzberg, S.L.; White, ri H · Oin H · Vamathevan I · Gill I · Scarl;	E.K.; Hait, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. Oin. H.: Vamathovan. T.: Gill. T.: Scarlato. V.: Masignani. V.: Disza. M.
Science		9-1815,	2000			
A; Autho	rs: Grand	1, 6.;	Sun, L		Smith, H.O.;	A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A; Title	: Complet	e genor	ne sedn	enc	e of Neisseria	A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Refer	ence numb	er: A8	1000; M	OID	:20175755	
A; Acces:	A; Accession: GBL133	133				
A; Status	A;Status: preliminary	inary				
A Resid	A.Moiecuie cype: DNA A.Residues: 1-591 <fft></fft>	1 < TET.	,			
A; Cross	A; Cross-references: GB: AE002450;	es: GB:	: AE0024	50;		GB:AE002098; NID:q7226229; PIDN:AAF41395.1; PID:q722
A; Exper	A; Experimental source: serogroup	ource:	serogr	dno.		28
C; Genetics:	C; Genetics:					

us-09-700-293-4.rpr

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Rifleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage Godacyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Scott, 496-512, 1995
A;Authors: Gaehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Authors: Gnebm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Accession: I64138
A;Acteus; mucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-298 ATIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: D82671
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Ayltitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MuID:20365717
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:U32846; GB:L42023; NID:91574588; PID:91574589; TIGR:H11732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)
C.Species: Haemophilus influenzae
C.Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C.Accession: 164138
       471 GSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGL 530
                                              531 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQ 590
                                                                                                                                                                             61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK- 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 DQGGKSVTFALAKDLDVKTAKVSDTLTIGGNTPAAGGATPKVSITSTADGLKLAK---GT 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.1%; Score 605; DB 2; Length 298; Best Local Similarity 45.9%; Pred. No. 44.46-23; Matches 145; Conservative 42; Mismatches 93; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2249 probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2249 c; Species: Nothman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491. A; Accession: A81888 A; Status: preliminary A; Molecule type: DNA A; Molecule type; DNA A; Molecule t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8;
481 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM 540
                                                                                                                                                                                                                                                                             421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 480
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84.4%; Pred. No: 1.7e-114;
tive 30; Mismatches 45; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                         541 MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
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                                            A:Cross-references: 1-209 < S.M.
A:Cross-references: G1-8003982; GB:AE003849; NID:g9106554; PIDN:AAFB4338.1; GSPDB:GN001
A:Experimental source: strain 9a5c
A:Experimental source: strain 9a5c
A:Experimental source: strain 9a5c
B:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm J.D.; Unqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigt Chado, M.A.; Madeira, A.M.B.N.; Madeira, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmis, E.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawasak, A.J. thuchors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A.Contents: annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGFNAGDKVISHVAVGMADTDAVNVSQLKQAVQSVTVKATRYYSTNDGGTQGGNYDGDGA 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGSKAIAAGVGTQASGEGAAAVGSGAAASGKGSTAIGRNAIASADGSVALGDGAKDGGRG 1798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----NFTYSLKKDLTDL-----TSVGTEKLSFSAN----GNKVNITS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DT------KGLNFAKETA----GTNGDTTVHLNGI-----GSTLTDTLLNTGA--T 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TVS-----KDDQGNITVMYDVNVG-DALNVNQL----QNSGWN 391
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13.1%; Score 393; DB 2; Length 2059;
Best Local Similarity 24.3%; Pred. No. 1.4e-11;
Matches 173; Conservative 93; Mismatches 216; Indels 230;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2059 <SIM>
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probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova C; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AC0976
                                                                                                                                                                                                                                                                                                                        R; Parkhill; J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Tille: Complete genome sequence of a multiple drug resistant Salmonella enterica se A; Reference number: AB0502; PMID:11677608
A; Accession: AC0976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1107 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQEEDLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSGTNKITNVAAGEIASDSTDAINGSQLYETNMLISQYNESISQLAGDTSETYITENGTG 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  685 AQDAVIVRQLQNAIGAVITIPIKYYHANSTEEDSLAVGIDSLAMGAKIIVNADAGIGIGL 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTLVMADAINGIAIGSNARANHANSIAMGNGSQTTRGAQTDYTAYNMDTPQNSVGEFSVG 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEDGQRQITUVAAGSADTDA---VNVGQLKVTDAQVSRNTQSITNLNTQVSNLDTRVTNI 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TLSVDGDA 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFAKETAGTNG----DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSEDSTDAVNGSQLYETNQKVDQNTSAIAD--INT-SITNLGTDALSWDDEEGAFSASHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VAVSELTRNHTKRASATVKTAVLATLLFATVQASANNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 NLKIKQNGT---NFTYSLKKDLTDLTSVGTEKL-----SFSAN--GNKVNITSDTKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNAGWNIKGVKPGTTASDNVDFV---RTYDT-----VEFLSADTKTTVN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 12.6%; Score 378; DB 2; Length 1107; Best Local Similarity 21.0%; Pred. No. 3.6e-11; Matches 178; Conservative 103; Mismatches 225; Indels 342;
----SSVSLGAGADAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSSGKVISGNVSPSKGKMDETVNINAG ----NNIEITRNGKNI-
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A; Molecule type: DNA
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OY 179 LNGIGSTLIDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAG-WNIKGVKPGTTASD- 236		RESULT 7  A86036  Probable adhesin 25029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Date: 16-Feb-2001 #sequence change 14-Sep-2001 C;Date: 16-Feb-2001 #sequence of change 16-Feb-2001 #text_change 14-Sep-2001 C;Date: 16-Feb-2001 C;Date: 16-Feb-2	Ouery Match  Best Local Similarity 24.7%; Pred. No. 3.1e-10; Matches 145; Conservative 78; Pred. No. 3.1e-10; Matches 145; Conservative 78; Mismatches 228; Indels 136; Gaps 22;  QY 121 NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVN-ITSDTKGLNFAKETAGTNGDTTVHL 179  Db 1022 NATNMANIEONTQIINQLAGNTDATYIOENGAGINYVRTNDDGLAFNDASAGGVGATAIGY 1081  QY 180 NGIGSTLTDTLLNTGA-TTNVTNDNVTDDE 208  Db 1082 NSVAKGDSSVAJGGGSXSDVDTGIALGSSSVSSKYIAKGSRDTSTTENGVVIGYDTTDGE 1141  QY 209 KKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVE 262  Db 1142 LLGALSIGDDGKYRGIINVADGSEAHDAVT-VROLQNAIGAVATTPTKXFHAN 1193  QY 263 SKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGE
Db 862 ENGIGDIUTTGSTKYFKTNTDGADANAQGADSVAIGSGSIAAAENSVALGTNSVADEANT 921  Qy 468 LNVGSKKDNKPVRITNVAPGVKEGDVINVAQLK	RESULT 6 A82615 Surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c) G:Species: Xylella fastidiosa C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C:Accession: A82615 R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa. A:Reference number: A82515; MUD:20365717 A:Note: for a complete list of authors see reference number A59328 below A:Accession: A62615 A:Settus: prefilminary A:Molecule type: DNA	A.Residues: 1-1190 (SINA) A.Residues: 1-1190 (SINA) A.Residues: 1-1190 (SINA) A.Cross-references: GB.ABC004017; GB.ABC003849; NID:99107083; PIDN:AAF84783.1; GSPDB:GN001 A.Experimental source: strain 9a5c Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; ARSimpson, A.J. G.; Rehach, F.C.; Arruda, P.; Acancago, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carrero, D.M.; Carrer, H. Sa-Neto, E.; Docena, C.; El-Dorry, H.; Fraincani, A.P.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr G.Ado, M.A.; Madeira, M.L.; Kemper, E.L.; Micki, C.F.M.; Marcko, C.E.M.; Miracca, E.C.; Myaki, C.Y.; F. Gri, Nunce, L. R.; Oliveira, M.B.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Myaki, C.Y.; F. Gri, Nunce, L. R.; Oliveira, M.A.; Modita, M.C.; de Oliveira, R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de Rus, de Rosa di. V. Rosa, R.G.; Santelli, R.V.; Sawasak A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.R.; Silva, M.R.; Vallada, M.H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A; Genetics: Anotation A.Reference number: A59328 A.Gontents: annotation A.Genetics: A.Genetics:	Ouery Match  12.4%; Score 371.5; DB 2; Length 1190;  Bast Local Similarity 23.5%; Pred. No. 8.1e-11;  Matches 167; Conservative 88; Mismatches 243; Indels 213; Gaps 28;  Qy 17 VAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEDGEDENZLDPVQRTVAV 71

Op	1194 STEEDSLAVGTDSLAMGAKTIVNGDKGIGIGYGAYVDANALNGIAIGSNAQVIHVNSIAI 1253	Db 1309GOLKVTDAOVSONTO-STTULDBRVTULDSRVTUIENGGGDIVTGSTKVFKTUPGGV 1365
Oy Dp	297 -NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSGTNV 348	386
Oy Dp	349 TFASGKGTTATVSKDDGGNITVMYDVNVGDALNVNQL 385	1366 DASAQGKDSVAIGSGSIAAADNSVALGTGSVATEENTISVGSSTNQKRITNVAAGKNATD 437 -IDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTN :::
8 8	386 QNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKN 436 1366 DASAAGKROVATGGGTAAAANGVATGGGGVAGFBWATGWGGGAAAGKROVATGGGGTAAAAAGKAGAAGKROVATGGGGTAAAAAGKAGGAGGAAGKROVATGGGGAAAGKROVATGGGGTAAAAAGKAAGKAAGKAAAGKAAAAAAAAAAAA	Db 1426 AVNVAQLKSSEAGGVRYDTKADGSIDYSNITLGG-GNGGTTRISNVSAGVNNNDVVN 1481  Qy 496 VAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIG 544
8 8 1	-IDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTN :::  ::	
3 6 7	AYNVAQLASSEAGGVKIDIAADGSIDISNIILGGG-GNGGIIKISNVSAGVNNNDVVN VAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIG 	542
8 6 8	1402 IAQLANGSVQETAQIIDQRAVEMDNALSKIESALSSGJASAMAMIGLENQATIFGASMASIG 1541 545 GGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591 11   -  -  -  -  -  -  -  -  -  -  -  -	AESOLT 9  RESOLT 9  Probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92) C.Specides: Yersinia pestis C.Specides: YerSioual #secuence revision 02-Nov-2001 #text change 02-Nov-2001
RESULT H91188	88 T.I.	C; Accession: AH0110 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
C;S	probable adhesin ECs4480 [similarity] - Escherichia coli (strain 0157:H7, substrain RIMC C; Species: Escherichia coli (C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001	Nature 413, 523-527, 2001 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
C; A gas	ccession: H91188 yasahi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Wawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.	A; Accession: AH0110 A; Status: preliminary A; Molecule type: DNA
A A A A A A A A A A A A A A A A A A A	DNA MES. 8. II-22. ZUOI A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A.Reference number: A99629; MUID:21156231; PMID:11258796 A.Accession: H91188	A:Residues: 1-658 <kur> A:Residues: 1-658 <kur> A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175 C:Genetics: A;Gene: YP00902</kur></kur>
	Actuals type: DNA Molecule type: DNA Residues: 1-1588 <hay> Cross-references: GB:BA000007; PIDN:BAB37903.1; PID:g13363955; GSPDB:GN00154</hay>	Query Match 11.0%; Score 331.5; DB 2; Length 658; Best Local Similarity 25.2%; Pred. No. 3.6e-09; Matches 132; Conservative 74; Mismatches 204; Indels 113; Gaps 22;
	ene: ECs4480	QY 101 GVLTAREITLKAGDNLKIKONGTNFTYSLKKDLFDLTSVGTEKLSFSANGNKVNITSDTK 160   : : ::
Z Ñ O	Query Match 12.1%; Score 363; DB 2; Length 1588; Best Local Similarity 24.7%; Pred. No. 3.1e-10; Matches 145; Conservative 78; Mismatches 228; Indels 136; Gaps 22;	161 GLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDV
Qy Dp	121 NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVN-ITSDTKGLNFAKETAGTNGDTTVHL 179 	219 LNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEV
Oy Dp	180 NGITDDE 208    1	318 ANGG-GVKYFHANSTQPDSVASGTNSVAIGPASLASGNAALASGAGAV 273 KIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGO 1 : 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
Oy Dp	209 KKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVE 262	Db 365 AIGDGAAASADGSVAIGQGSGDNGRGVENYIG
٥٧ و	SKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGE	TVSVGNTATGETRTVSNVADGLQATI KAVAGSSGKVISGNVSPSKGKMDETVNINAGNNI-EITRNGKNI
ço ç	-NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKETTVTSGTNV	Db 443IAASIVVVENNVSGLQNGTDGMFQVNNSSGLAKPSATGANSATGGAGSVASGNNS 497 Qy 450 VSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAFGVKEGDVTNVAQL 499
g &	1254 GNGSTTTRGAUTNYTAXNMDAPQNSVGEFSVGSADGQRQITNVAAGSADTDAVNV 1308 349 TFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQL 385	:  :

NuLINNRIDNVDGNARAGIAOAIATAGLVQAYIDGKSWAAIGGGTY 548  OUTET	0y 333 TGOADER 0y 333 TGOADER 0y 390 WNLD 0y 390 WNLD 0y 443 MTPOFES 0y 443 MTPOFES 0y 449 LKGVAQP 0y 499 LKGVAQP 0y 545 0y 546
A NOIYEKEWILSLICSWSVASHWITTH   1   1   1   1   1   1   1   1   1	Query Match         7.8%; Score 235.5; DB 2; Length 1091;           Best Local Similarity         23.1%; Pred. No. 0.00036;           Matches 144; Conservative 71; Mismatches 203; Indels 205; Gaps 35;           Qy 1 MRKTRIINMSALNAWVAVSELTRNHYRRASATVKTAVLATLLEATVOASANNEEGEEDL 60           :   1   :

Qy 275 G-AKTSVIK      : :   Db 280 GTANTTVV-	G-AKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRM- 324	QY 371 MYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAG 	425 1114
Qy 325KT Db 331 KNGGVAGN	KTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQG-NITVWYD 373 	QY 426 NNIEITRNGKNIDIATSWIPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRIINVA 485	485 1172
Qy 374 VNVGDALN           Db 385 VVEGKADN	VNVGDALNVNOLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN 433	QY 486 PGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAI 543	543 1226
Qy 434 GKNIDIAT         Db 425 GGT	GKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKRDNKPVRITNVAPGVKEGDV 493	Qy 544 GGGTYRGEAGYAIGYSSISDGGNWIIK	
QY 494 TNVAQLKG :    DD 465 DALMLEKG	TNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAG 553	RESULT 13 B43855	
Qy 554 YAIGYSSI   ::: Db 499 TLAGTTTL	554 YAIGYSSISDGGNWIIKGTASGN 576 499 TLACTTTLNNGAILTLSGKTVNN 521	high-molecular-weight surface-exposed protein - Haemophilus influenzae C.Species: Haemophilus influenzae C.Bate: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994 C.Accession: 1843855	194
RESULT 12 A43855		Arbate Indum, 5.1.; Defininger, 5. Infect. Immun. 60, 1302-1313, 1992 Arithe: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable	, nontypeable
high-molecular-wei C; Species: Haemoph C; Date: 10-Mar-199	high-molecular-weight surface-exposed protein HWW1 - Haemophilus influenzae C;Species: Haemophilus influenzae C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999	A;Reference number: A43855; MUID:92192797 A;Accession: B43855 A;Status: preliminary	
C.Accession: 4430. R:Barenkamp, S.J.; Leininger, E. Infect. Immun. 60, 1302-1313, 1992 A:Title: Cloning, expression, and D	C. McCassion: A. 303.7. Leininger, E. Infect. Immun. 60, 1302-1313, 1992. A. Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Ha	A;Molecule Type: DNA A;Residues: 1-1477 <bar> A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:89237, NCBIP:89240)</bar>	
detella pertussis. A:Reference number: A A:Accession: A43855 A:Status: preliminary A:Molecule type: DNA	detella pertussis. A;Reference number: A43855; MUID:92192797 A;Accession: A43855 A;Status: preliminary A;Molecule type: DNA	Query Match Best Local Similarity 22.6%; Pred. No. 0.0028; Matches 139; Conservative 92; Mismatches 231; Indels 152; Gaps	3 30;
A; residues: 1-1030 A; Cross-references A; Note: sequence i A; Note: sequence e	A;Cross-Treferences: GB:U00876; GB:M84616; NID:9475770; PIDN:AAA20527.1; PID:9475771 A;Cross-Treferences: GB:U00876; GB:M84616; NID:9475770; PIDN:AAA20527.1; PID:9475771 A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:89235, NCBIP:89239)	QY 11 SALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQR 67 11:1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	67 878
Query Match Best Local Similarity		QY 68 TVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTN 124 :	124 925
Qy 40 ATLLFATV 133, C	40 ATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNE 99	QY 125 FTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKET 168 i : : :	168 976
	KGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSD- 158	QY 169 AGTNGDTTVHLNGIGSTLIDTLLNTGATTNVTNDNVTDDE 208 i   i	208 1035
159	KGIVAKKNIIFEGGGNIFEGSRKAVTELEGNVTINNANVTLIGSDF 866 TKGLNFAKETAGTNGDTTVHLNGIGSTLIDTLLNTGAT-TNVTN 201 	QY 209 KKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGK 268	268 1086
202		QY 269 KTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGL-VTAKEVIDAVNKAGWRMKTT 327 S.: : : :         ::         :	327
QY 262 ESKDNGKK	TYRTIISGNITNKNGDLNI GENGSSTDEGEGLVTA	OY 328 TANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVUCLON   :   :     :     :     :     :     :     :     :     :     :     :     :	387 1186
311	SGNITV  :	QY 388 SGWNLDSKAVAGSSGKVISG*-NVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTP :   :   :     :   :   :     :     :   DD 1187TVDLTTKSGSKIEAKSGEANVTSATGTIGGTISGNTVNVTANAGDLTVG	445 1235
Db 1023DATN		QY 446 QFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVA 503	)3

:	Dy 99 DTGSIGVLINGEGATVSNINGENTATIONS TRANSPORTED TO STATE OF THE STATE	RESULT 15  Probable adhesin hmwA [imported] - Yersinia pestis (strain C092)  C; Species: Yersinia pestis C; Species: Versinia pestis R; Parkhill, J; Wren, B W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, R; Parkhill, J; Wren, B W.; Thomson, N.R.; Titball, R.W.; Davis, P.; Dougan, II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre A; Title: Genome sequence of Yersinia pestis, the causative agent of plague. A; Reference number: AB0001; MUD:21470413; PMID:11586360 A; Accession: A;	Ouery Match  236; Gaps  40; Best Local Similarity 20.5%; Pred: No. 0.0048; Caps
:	change	Althle: The Complete genome sequence of Escherichia coli K-12. Althle: The Complete genome sequence of Escherichia coli K-12. Althle: The Complete genome sequence of Escherichia coli K-12. Althle: The Complete genome sequence of Escherichia coli K-12. Althle: The Complete genome sequence of Escherichia coli K-12. Althle: The Complete genome sequence not shown; translation not shown Almolecule type: DNA Almolecule type: DNA Althle: The Complete genome strain K-12, substrain MG1655 Althle: The Complete genome strain K-12, substrain MG1655 Althle: The Complete genome coling and sequence not shown; translation not shown Almolecule type: DNA Althle: The Complete genome coling genome shown; translation not shown Almolecule type: DNA Althle: The Complete genome coling	Query Match . 7.4%; Score 221; DB 2; Length 2020; Best Local Similarity 23.6%; Pred. No. 0.0041; Matches 167; Conservative 75; Mismatches 230; Indels 236; G SanneBedelLyLDPVQTVAULINNSDREGTGEKEKVEENSD

1137	329	1187	370	1247	399	1307	417	1367	460	1427	520	1486	576	1546			
		GRNIDINGSSAGTGDVYFTNVELNATAGNVSIYAETKTALS	330NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITV	TSLNAVLSLGGNNSIKAQNGWLIGKAFNTTQGAGIGFRANSSLSVDGNIILKGETEGVGA	371MYDVNVGDALNVNQLONSGWNLDSKAVAG	TRKGIDFYGANTLNIIKGSQLSLLGENKGAQDTAGGNGISYTSLAKLTVNNNGSLKMEGR	SSGKVISGNVSPSKGKMD		ETVNINAGNNIEITRNGKNIDIA-TSMTPQFSSVSLGAGADAPT	1368 VHLFSAEHRIDRINVTGSSTHAEGLRISGNAAIVDTTLTGKSINGSGVKIDSLPGSSVVT	LSVDGDALNVGSKKDNKPVRITUVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAG		IAQAIATAGL-VQAYLPGKSMMAIGGGTYRGEAGYAIGYSS-ISDGGNWIIKGTASGN	1487 LLILQGVATTGTGTGTKLNGNNDLSNTSLNSSAVDGTALDITGPLANQGNVILNGTASGS	SRG 579	GIG 1549	
1090	274	1138	330	1188	371	1248	400	1308	418	1368	461	1428	521	1487	577	1547	
qq	Qy	qq	ογ	qq	δλ	qq	Οy	qq	Οy	qq	Qy	qq	ολ	qa	δλ	QQ	

Search completed: September 5, 2002, 10:24:38 Job time: 245 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

September Run on:

5, 2002, 10:31:01; Search time 19.11 Seconds (without alignments) 1197.449 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-700-293-4 3003 1 MNKIXRIIWNSALNAWVAVS.....TASGNSRGHFGASASVGYQW 591

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	m	-	Q03155 escherichia	P32051 escherichia	P16466 proteus mir				P25927 salmonella	Q9kka3 r outer mem		-	P45355 haemophilus		P45354 haemophilus	P35827 campylobact	-	ğ	P38536 t amylopull	×	Q52657 rickettsia		O30611 pseudomonas		P35828 caulobacter					O9phw6 campylobact		Q9rb65 chlamydia p	Φ.
SUMMARIES		QI	AG43_ECOLI	YDBA_ECOLI	AIDA_ECOLI	YDEK_ECOLI	HLYA_PROMI	OMPB_RICRI	HLYA_SERMA	OMPA_RICRI	BIGA_SALTY	OMPB_RICCN	OMPB_RICTY	Y741_CHLMU	HXA3_HAEIN	OMPB_RICJA	HXA2_HAEIN	SLAP_CAMFE	YPJA_ECOLI	WAPA_BACSU	APU_THETU	ICEN_XANCT	OMPA_RICCN	YMJB_CAEEL	ICEK_PSESX	OMPB_RICPR	SLAP_CAUCR	120K_RICRI	SLAP_LACAC	FLIC_SHIFL	MRSP_STAAU	FLID_CAMJE	ALYS_ENTFA	PM10_CHLPN	FLIC_ECOLI
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		Score	235.5	221	212.5	210	207.5	201	191.5	191	189.5	186,5	185	183	182	181	180.5	180.5	180.5	180	176	175.5	175	174	167.5	167	166	165.5	164.5	163	161.5	159.5	159	159	158
	Result	NO.	1	7	m	4	ស	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26		28				32	33

P44969 haemophilus	P45384 haemophilus	P50493 plasmodium	033479 pseudomonas	P46949 saccharomyc	P06620 pseudomonas	P20676 saccharomyc	Q06974 salmonella	P56867 deinococcus	P15345 caulobacter	Q9zkw5 helicobacte	P46590 candida alb
IGAO_HAEIN	IGA2_HAEIN	PVDB_PLAKN	ICEV_PSESX	YG4A_YEAST	ICEN_PSESY	NUP1_YEAST	FLIC_SALON	HPI1_DEIRA	FLEY_CAUCR	VACA_HELPJ	ALS1_CANAL
П	-	-	Н	-	Н	Н	-	Н	-	<b>,</b>	п
1694	1702	1153	1196	817	1200	1076	507	948	954	1288	1260
5.3	5.3	5.5	5.5	5.5	5.2	5.2	5.1	5.1	5.1	5.1	5.1
158	158	157.5	157	156.5	156	155.5	154.5	154.5	154.5	154	153.5
34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

AG43_ECOLI STANDARD; PRT; 1039 AA. ID AG43_ECOLI STANDARD; PRT; 1039 AA. AC P39180; P76360; P75614; P97241; Q46771; DT 01-FEB-1995 (Rel. 31, Created)	01-NOV-1997 (Rel. 35,		DE ANTIGEN 49 PIECUISOI (A645) (FIGUING PIOCEIN).			Escherichia.												RN [2]		RC STRAILERIZE STR	KA MEDDINE=9/201006; Fubmed=909/040; RA Troh T., Aiba H., Baba T., Fuilta K., Havashi K., Inada T., Isono K.,	Kasai H. Kimura S. Kitakawa M. Kitagawa M. Makino K. M.	RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,				"A 460-kb DNA sequence of the Escherichia coli K-12 genome					STRAIN=ML 308-225;	KA HENDELSON 1.K., OWEN F.; DI S.hmitted (INN-1007) to the DMDI Conbent Antehases	[4]						43, a unique protein complex associated with the outer membran	Escherichia coli.";		. [2]		STRAIN=KIZ FMGZ:		AA MEDLINE=9/449/3/ PUDMed=9/29/040/	RA Link A.J., Robison K., Church G.M.;
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228 GTANTIVV-----YAGGDQIVHGHALDITILNGGYQYVHNGGTASDIV--VNSDGWQIV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 KNGGVAGNTIVN-QKGRL-QVDAGGTATNVTLKQGGALVTSTAATVT---GINRLGAFS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 IKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTV 177
                                                                      80 --TNGMISTGLEYGPDNEANTGGWWQDGGTANKTTVTSG--GLQ-RVNPGGSVSDTVI 134
                                                                                                                                                                                         135 SAGG-GOSLOGRAVNITILNGGEQWMHEGAIATGTVINDK--------GWQ 175
                                                                                                                                                                                                                                                      225 IKGVKPGTTASDNVDFVRT-----YDTVEFLSADTKTTTVNVESKDNGKKTEVKI 274
                                                                                                                                                                                                                                                                                  275 G-AKTSVIKEKDGKLVTGKDKGENGSSTDE----GEGLV----TAKEVIDAVNKAGWRM- 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 -----KTTTANGQTGQADKFETVTSGTNVTFASG----KGTTATVSKDDQG-NITVMYD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 VNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 GKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDV 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 G----GTATT----VSMGNGG---VLLADSGAAVSGTRSDGK-----AFSIGGGQA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 INVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 DALMLEKGSSFTLN-----AGDTATDTT-------VNGGLFTARGG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasal H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Mashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takendo K., Takenchi Y., Wada C., Yamanoto Y., Horiuchi T.; "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                         HLNGIGSTL----TDTLLNTG-----ATTNVTNDNVTDDEKKRAASVKDVLNAGWN 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=KI2 / MG1655;
MG1655;
MG167617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
Mau B., Shao Y.;
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT, 2003 AA.
P3866; P76087; P76085; P76859; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12;
MEDLINE=97251357; Pubmed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     554 YAIGYSSISDGGNWIIKGTASGN 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 TLAGTTTLNNGAILTLSGKTVNN 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                               FEMS Microbiol. Lett. 149:115-120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YLDPVQRTVAVLIVNSDKE---GTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLK 117
                                                                                                   MEDLINE-97257509; PubMed-9103983; Handerson I.R., Meehan M., Owen P.; Handerson I.R., Meehan M., Owen P.; Hantigen 43, a phase-variable bipartite outer membrane protein, determines colony morphology and autoaggregation in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71; Mismatches 203; Indels 205; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LNTCYRLVWNHMTGAFVVASELARARGKRGGVAVALSLAAVTSLPVLAA------DI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNLVHTS -> MNLIYNA (IN STRAIN ML 308-225).
QGT -> LGA (IN STRAIN ML 308-225).
Q -> L (IN STRAIN ML 308-225).
Q -> L (IN STRAIN ML 308-225).
S -> I (IN STRAIN ML 308-225).
ETV -> TIN STRAIN ML 308-225).
ETV -> TIN STRAIN ML 308-225).
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                                                                                                                                                                                                                                                                                               FUNCTION AS AN ADHESIN.
SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLOLD 43 BETA CHAIN

K -> N (IN STRAIN ML 308-225).

T -> FF (IN STRAIN ML 308-225).

T -> K (IN STRAIN ML 308-225).

W -> L (IN STRAIN ML 308-225).

A -> T (IN STRAIN ML 308-225).

A -> T (IN STRAIN ML 308-225).

A -> T (IN STRAIN ML 308-225).

B -> V (IN STRAIN ML 308-225).

C -> V (IN STRAIN ML 308-225).

B -> V (IN STRAIN ML 308-225).

C -> K (IN STRAIN ML 308-225).

C -> C (IN STRAIN ML 308-225).
                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED. SIMILARITY: TO ADHESIN AIDI-I AND TO BORDETELLA PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.8%; Score 235.5; DB 1; Length 1039; 23.1%; Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTIGEN 43 ALPHA CHAIN. ANTIGEN 43 BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Complete proteome.
in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AE000291, AAC75061.1; ALT_INIT.
EMBL, D90839; BAAL5825.1; ALT_INIT.
EMBL, D90839; BAAL5832.1; ALT_INIT.
EMBL, U24429; AAR47869.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 VVHPGETVNGGTLANHDNQIVFGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106841 MW;
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1039 AA;
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us-09-700-293-4.rsp

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579 DTGSIGVLINGEGATVSNTGDVNVS-NEATGFSITTNSGKVSLAGSMQVGDFSTGVDLNG
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                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | || || :|| ::|: :| || || SFNN-----DVILDKTERTLIRDSVFTYTENADGTISLQDSNGRRATINLWQIDEANNT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WAV-----YFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGEGLVTAKE-----VIDA----VNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFAS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 VAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSM-TPQFS----- 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E-----KLSFSANGNKVNITSDT----KG-----LNF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SANNEEQEEDLYLDPVQRTV----AVLIVNSDKEGT------GEKEKV-----EENSD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 VALEGVSADGATKWQYNHNCELVI-----TGDNATVNNNG------KTTVDGKDSTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKETAGINGDITVHLNG-----IGSILIDILLNTGATINVINDNVIDDEKKRAASVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 EGESTITNGGTGTQINGDDATANNNGKTTVDGKDSTGTEINGNNGKVIQD-----GDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 GKGTTATVSKDD-----QGNITVMYDVNVGDALNV----NQLQNSGWN--LDSK----A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 VLNAGWNIKGVKPGTTASDNVDFVRTYDTVEF-LSADTKTTTVNVESKD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236;
                                                                                                                      Moszer I., Glaser P., Danchin A.; "Multiple IS insertion sequences near the replication terminus Facherichia coli K-12 ";
                                                                                                                                                                                                             -i- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG (AC P25928).
-i- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING THIS PROTEIN IS INTERRUPED BY A HYBRID IS2D/IS30C ELEMENT BETWEEN AMINO ACIDS 839 AND 840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.4%; Score 221; DB 1; Length 2003; 23.6%; Pred. No. 0.0015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome.

CONFLICT 489 489 I -> V (IN REF. 2).

CONFLICT 495 495 I -> V (IN REF. 2).

SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000237; AAC74483.1; ALT_SEQ. EMBL; AE000237; AAC74487.1; ALT_SEQ. EMBL; D90778; BAA15009.1; ALT_SEQ. EMBL; D90778; BAA1880.1; ALT_SEQ. EMBL; D90779; BAA1881.1; ALT_SEQ. EMBL; X62680; -; NOT_ANNOTATED_CDS. ECGENE; EG11307; ydbA.
                                                                                          MEDLINE=92190338; PubMed=1665988;
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                                             OF 464-2003 FROM N.A.
                                                                                                                                                                                         Biochimie 73:1361-1374(1991).
DNA Res. 3:363-377(1996).
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                                                                                                                                                                   Escherichia coli K-12
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Matches 167; Conserv
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                                                                                                                                                                                                      698 VYGSDNNVTLDGKLTVVSDSEVTSROSNLFDGSAE-----KTSGLVVIGDGNTVNMNG 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escherichia coli strain 2787 (0126:H27), is synthesized via a precursor molecule.";
MOI. Microbiol. 6:1539-1546(1992).
-i- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
                                           638 NNNSVILAAKDLKVVGQKATGINVSGDANTVNITGNVLVDKDKRADNAAEYFFDPSVGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SVSLGA-----GADAPTLSVDGDALNV---GSKKDNKPVRITNVA-----PGV---
                                                                                                                                     ---KEGDVTNVAQLKGVAQN-LNNRIDNV-DGNARAGIAQAIATAGLV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1286;
                                                                                                                                                                                                                                                                                                                  1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;
                                                                                                                                                                                                                                                                       532 -QAYLPGKSMMAIGGGTYRGEAGYAI-----GYSSISDGGNWIIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94; Mismatches 274;
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11.1%; Pred. No. 0.0023;
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PIR: S28634; S28634.
Call adhesion; Signal; Outer membrane; Plasmid.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADHESIN AIDA-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
STRAIN=2787 (0126:H27);
MEDLINE=92326638; Pubmed=1625582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
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181 QRV -- SSGGVASNTINSSG---AQNILSEEGAISTHISSGGNQXISAGANATETIVNSG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                           255 KTTTVNVESKDN----GKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 TDTTVNSGGNQNISSGGIVSETTVNVSGTQNIYSGGSALSANIKGS------329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 INSGGTAPVQNSVVVTRTVSSAAKPFDAEVYSGGKQTVYLWRGIWYSNFLFAVWSMFPGT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 KEGDVTNVAQLKGVAQNLNNRIDNVDGNARA-----GIAQAIATAGLVQAYLPGKSMMAI 543
                                                                                                                     142 EKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN-----GIGSTLTDTLLNTG 194
                                                                                                                                                                                                                                                                            195 ATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADT 254
                                                                                                                                                                                                                                                                                                                                                           236 GFQRVNSG-----AVATGTVLSGG--TQNVSSGGSAISTSVYNSGVQTV-FAGATV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 KEVIDAVNKAGWRMKTTTANG-----QTGQADKFETVTSGTNVTFASG------KGT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 ----QIVNSEGTAINTLVSDGGYQHIRNGGIASGTIVNQSGYVNISSGGYAESTIINSGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATVSKDDQGNITVMYD---VNVGD-ALNVNQLQNSGWNL------DSKAVAGSSG--K 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VISGNVSPSKGKMDETVNINAGN --- NIEITRNGKN ------IDIATSMTPQF 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS---VSLGAGADAPTLSVDGDALN------VGSKKDNKPVRITNVAPGV 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562 TDGTVLNSGGLQAVSSG-----GKASATVINEGGAQFVYDGGQV----TGTNIK-- 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97251357; PubMed=9097039; Maha H., Inada T., Isono K., Itoh T., Abba H., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Rasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Mixi T., Mizobuchi K., Mori H., Mori T., Motomura K., Makano K., Makamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundarama S., Tagami H., Takeda J., Takeduchi Y., Horiuchi T.;
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STRAIN-12 / MG1655;
MEDLINE-9742617; Pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plundo-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             506 ASGANVNLSGRLNAFAGNVVGTILNQEGRQYVYSGATATSTVGNNEGREYV----LSGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDEK_ECOLI STANDARD; PRT; 1325 AA.
P32051; P76140; P77168;
01-CCT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
YDEK OR ORFT OR B1510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544 GGGTYRGEAGYAIGYSSISDGGN 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        607 NGGTIRVDSGASALNIALSSGGN 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GIGST--LTDT-----LLNTG----ATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVK 229
                                                              [3]
SEQUENCE OF 595-1325 FROM N.A.
MEDLINE-94100243; PubMed=8274505;
Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
"An Escherichia coli gene showing a potential ancestral relationship to the genes for the mitochondrial import site proteins ISP42 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 --TNIDTDVAYDAYLVGWYGTGVLNILAGGN-ASLTTITTSV-----IGANEDSEGTVN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTE-----VKIGAKTSVIK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKDGK-LVTGKDKG------ENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 EKGGEWLIKNNDSSIEFQIGNQGTGEATIREGGLVTAENTIIGGNATG----IGTLNVQ- 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 -GTVNVEGEDSVLTTELFEIGSYGTGSLNIT----DKGYVTSSIVAILGYQAGSNGQVVV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 GQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALN--VNQLQNSGWN 391
                                                                                                                                                                to the genes for the mitochondrial import site proteins ISP4.2 and MOM38."; Blochlin. Blochlys. Acta 1153:345-347(1993).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 -----TLGVLLALS---GSASGASLEVDNDQI-------71
                                                                                                                                                                                                                                               (Potential).
SIMILARITY: TO E.COLI YFAL.
SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
"A 570 kb DNA sequence of the Escherichia coli K·12 genome corresponding to the 28.0-40.1 min region on the linkage map."; DNA Res. 3:363-37(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 210; DB 1; Length 1325; 22.9%; Pred. No. 0.0032; tive 72; Mismatches 266; Indels 160;
                                                                                                                                                                                                                                                                                                        ISPA2 AND MOM38.
-!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL LIPOPROTEIN YDEK.
N-ACYL DIGLYCERIDE (POTENTIAL).
N -> K (IN REF. 3).
M -> S (IN REF. 3).
WW. 26A3A066FA19AD7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Membrane; Lipoprotein; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S34315; S34315.
EcoGene; EG11780; ydeK.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000248; AAC74583.1; --
BEBL; D90793; BAAL5190.1; ALT_INIT.
BEBL; N90794; BAAL5197.1; ALT_INIT.
EMBL; X73295; CAA51730.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1317 1317
1325 AA; 136514
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Matches 148; Conservative
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884
1317
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.

1. SUBCELLULAR LOCATION: Outer membrane.

-1. MISCELLANEDUS: THE CONSRIVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION.
                                                                                                                                         424 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKD-NKPVRIT 482
                                                                                                                                                                                    451
                                                                                                                                                                                                                                                   452 IGVAGVGINISDGG--KFVSQNITFLGDKASGIGTLNLMDATSSFDTVGINVGNFGSGI 509
283 -DQDSVITVRRLYNGYFGNG---TVNISNNGLINNKEYSLVGVQDGSHGVVNVTDKGHWN 338
                                                             423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uphoff T.S., Weich R.A.;
"Nucleotide sequencing of the Proteus mirabilis calcium-independent
"Nucleotide sequencing of the Proteus mirabilis calcium-independent
"Nucleotide sequencing of the Proteus sequence similarity with the
Serratia marcescens hemolysin genes (shlA and shlB).";
J. Bacteriol. 172:1206-1216(1990).
-I- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                        483 NVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLP--GKSM
                                                                                                 339 FLGTGEAFRYIYIGDAGDGELNVSSEGKVDSGIITAG---MKETGTGNITVKDKNSVITN
                                                                                                                                                                                 LGTNLGYDGHGEMNISNQGLVVSNGGSSLGYG----ETGVGNVSITTGGMWEVNKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1577 HEMOLYSIN.
AA; 165869 MW; 175975E0C924B2D9 CRC64;
                                                                                                                                                                                                                                                                                                        MAIGGGTYRGEAGYAI -----GYSSISDGGNWIIKGTASGNSR 578
                                                                                                                                                                                                                                                                                                                               L-----DSKAVAGSSGKVISGNVSPSKGKMDET----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1577 AA
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Hemolysis; Toxin; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN-ISOLATE 477-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90170827; PubMed-2407716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M30186; AAA25657.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hemolysin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                HLYA_PROMIP
P16466;
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------EGTGEKEKVE-----ENSDWAVYFNEKGVLTAREITLKAGDNLK 117
                                                                                                                                                                                                                                                                                                                                         GGGONKNNNNOOOVSHATOLTADGOLLLAADNNVNITGSQVKGNQGAFVK--TTQGDVVI 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650 IKSADKLGIHSLGDINVKSAQQVTKIDDEKTSLAITGHAKEVEDKQYSAGFHITHTTNKN 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 SVSLGAGA------NKPV 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R-----ITHNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA 533
                                                                                                                                                                                                                            KETAG-----GIGSTLTDTLL---NT 193
                                                                                                                                                                                                                                                                ELTAGKDLGLDAQGSITAQGAKLHANENVLVNAKDNINLNVQKTNNDKTVTDNHVMWGGI 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      768 -NTDITISGGFS---YTGGVDKVGSKADFQYD-KQHTQTEVTKNRGSQTEVAGDLIITAN 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTGKDK-----GE-NGSST----DEGEGLVT---AKEVIDAVNKAGWRMKTTTANG
                     306 ITVNNSGSSQTLTKTELKGKNI--TLVASSHNQIKASDLMGDDITLQGADLTIDGKQLQO
                                                                                                 MEDLINE-92167802; PubMed-1724278; Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.; "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor.";
                                                                                                                                                                        424 INAN------KDIHINGLVEKESRSENGNKRNHTSRLESGSWSNSHQTETLKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTGQADKFETVTSGTNVTFASGKGTTATVS - - KDDQGNITVMYDVNVGDALNVNQLQNSG
LTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSDK---
                                                                                                                                                                                                                                                                                                        GATTNVTNDN------VKPGTTASDNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          710 TSTETEQANSTISGANVDLQANKDVTFAGSDLKTTAGNASITGD-NVAFVSTENKKQTD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 WNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRN-GKNIDIATSMTPQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               823 KDLLHEGASHHVEGRYQESGENIQHLAVNDSETSKT--DSLNVGIDVGVNLDYSGVTKPV
                                                                                                                                                                                                                                                                                                                                                                                 240 FVRTYDTVEFLSAD-----TKTTTVNVESKDNGKKTEVKIGAKTSVIKEKD----GKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsleae; Rickettsia.
                                                                                                                                                   118 IKONGTNFTYSLKKDLTDLTSVG-TEKLSFSANGNKVNITS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia rickettsii.
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Q53047;
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32;

Gaps

Length 1577; Indels 193;

6.9%; Score 207.5; DB 1; 22.3%; Pred. No. 0.0052; iive 86; Mismatches 258;

Best\_Local Similarity 22.3 Matches 154; Conservative

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                    113 GDNLKIKQNGTNFTYSLKKDLTDLT--SVGTEKLSFSANGNKVNITSDTKGLNFAKETAG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 TNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 GTTASDNVDFVRTYDTVEFLSADTKTTTVN-----VESKDNGKKTEV--KIGAKTSV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.7%; Score 201; DB 1; Length 1654;
22.6%; Pred. No. 0.011;
Ive 83; Mismatches 282; Indels 196; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 LLLNTANNLAVTVSEDTILGFITNVVHNAHSFNLTLNAG---KTLTITGQGVTNAQAAAT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 NEEQEEDLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 GDNAVI-ANGVNGTLNVTNGFIQVSNKSFATVKAINIADGQGIIFNTDANNANTLNLQA- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 --GGTTINFTGTDGTGRLVLLSKHAA--ATNFNITG------SLGGNLKGVIE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 FNIVA-----VDGQLTANAGAANAVIGTNNGAGRAAGFVVSVDNGKVATIDGQVYAKDMV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 IKEKDGKLVTGK------DKGENGS------STDEGEGLVTAKEVI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 IQSAN---ATGOVNFRHIVDVGADGTTAFKTAASKVTITQDSNFGNTDFG-NLAAQIKVP 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 DAV-----NKAGWRMKTTTANG--QTGQADKFETVTSGTNVTFASGKGT-- 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 NAITLIGNFTGDASNPGNTAG--VIFFDANGTLESASADANVAVTNNITAIEASGAGVVQ 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 ----TATVSKDDQGNITVMYDVNVGDALN--VNQLQNSGWNLDSKAVAGSSGKVISGNV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 SPSKGKM-----D-TRNGKNI----D 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 KDA SURFACE-EXPOSED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1334 1654 32 KDA BETA PEPTIDE.
1181 1188 POLY THR.
754 AA, 168184 MW; D7AB70EP7087F618 CRC64;
Mol. Microbiol. 5:2361-2370(1991).
[2]
                                                        STRAIN=R;
MEDLINE=90136087; PubMed=2515418;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR003858; rompA_rompB.
Pfam; PF02708; rompA_rompB; 1.
Antigen; S-layer; Cell wall.
CHAIN 1333 120 P
                                    SEQUENCE OF 279-1654 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X16353; CAA34403.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.7%;
Best Local Similarity 22.6%;
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439 IATSMTPQFSSVSLGAGADAPTLSVDG------DALNVGSKK---DNKPVRITN 483
                                                484 VAPGVKEGDV-----TNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAY 534
                                                                                                                                                                                                    535 LPGK----SMMAIGGGTYRGEAGYA-----IGYSSISDGGNWIIKGTASGNSRGH 580
                                                                                                                                                                                                                                                                                                                                                460 RNHTSSLRTGRWSNSDESESLKASELRSEGELTLKAGRNVSTOGAKVHAORDLTIDADNO 519
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WEDINE-BESSESST037; PubMed-1290200;
POOLE K., Schiebel E., Braun V.;
"Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol. 170:3177-3188(1988). FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serratia marcescens.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
6.4%; Score 191.5; DB 1; Length 1608;
Best Local Similarity 2.18%; Pred: No. 0.032; Indels 217;
Matches 15; Conservative 87; Mismatches 239; Indels 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN 31 1608 HEMOLYSIN.
SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hemolysis; Toxin; Outer membrane; Signal.
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NCBI_TaxID=615;
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P15320;
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us-09-700-293-4.rsp

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		Db 924 IGAQGGSSEKRSSSQAVVSSVQAGSIDINAKGEVRDQGTQYQASKG-AVNLTADSHRSE 982  QY 508NRIDNVDGNARAGIAQAIATAGIVQAYLPGKSMMAIGGGTVRGEAGYAIGYSS 560	RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;  RY A protective protein antigen of Rickettsia rickettsii has tandemly  RT repeated, near-identical sequences.";  RL Infect. Immun. 58:2760-2769(1990).  C FUNCTION: ELICITS PROTECTIVE IMMUNITY.  CC SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  S-LAYER WITH HEXAGONAL SYMMETRY.  CC PTW: GLXCOSYLATED (PROBABLE).  CC PTW: GLXCOSYLATED (PROBABLE).  CC SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  CC SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GGAVIKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANNGI-VTFTGNSTVTG 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1123 NLTDNASAVTFTN--PVVVTGAIDNTG-----NANNGIVTFTGNSTVTGDIGNTNALA 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1074 TGNANNGIVTFTGNSTVTGNVGN-----TNALATVNVGAG----LLQVQGGVVKANTI 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 TVNINAG-----NNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDAL--NVG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKKDN-KPVRITUVAPGVKEGDVTUVAQLKGVAQNLNNRIDNVDGNARA----GIAQAIA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T----AGL-VQAYLPGKSMMA-----SIS 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 NEKGYLTAREITLKAGDNLKIKQNGTNFTYSLKK---DLTDLTSVGTEKLSFSAN----G 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 NKVNITSDTKGLNFAKETAGTN-------GDT--TVHLNGIGSTLTDTLLNT- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 ------GATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    880 SLATISVGAGTATLGGAVIKATTTKLTN----AASVLTLTNANAVLTGAIDNTTGGDNV 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 DEVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.4%; Score 191; DB 1; Length 2249;
24.4%; Pred. No. 0.051;
tive 56; Mismatches 212; Indels 172;
                                                                                                                                                                                                                 OUTER MEMBRANE PROTEIN A.
13 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                             Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein. SIGNAL
                                                                                                                                                                                                                                             A (TYPE I).
C (TYPE II).
C (TYPE II).
E (TYPE II).
G (TYPE I).
I (TYPE I).
J (TYPE I).
L (TYPE II).
M (TYPE II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563 DGGNWIIK-----GTASGNSRGH---FGASASVG 588
                                                                                                                                   PIR; A41477; A41477.
InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224333
                                                                                                                     EMBL; M31227; AAA26380.1; -
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Best Local S
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29;

Gaps

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280 VIKEKDGKLVTGKDKGENGSSTDEGEGLVT--AKEVI--DAVNKAGWRMKTTTANGQTGQ 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 NVAQLKGVAQNLNNRIDNVDGNARAG----IAQAIATAGLV------QAYLP---- 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 GDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 GDNATIKNTGTS-----DISGAGSTGT----VIDGNNARVNND-------480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 GDTTVHLNGIGSTLT-DTLL--NTGATT-----NVTNDNVTDDEKKRAASVKDVLN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 GDMTITDGGTGGHITGDNVVIDNAGSTTVSGADATALYIEGDNAL-----VIN 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 AG-WNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 529 EGNQTISGGAVGTRIDGD----- 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 GWNLDSKAVAGSSGKV-ISGNVSPS-----KGKMDETVNINAGNNIEITRNGK-NI 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         537 --GKSMMAIGGGTYRGEAG-----YAI----GYSSISDGGNWIIKGTASGNSRGHFGA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  835 TYNALLMADGEGTSIENKGDITSHGVYSVIRADNGSEVSNSGDILVYATSSNSSEDRAAI 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OWPE_NICCN STANDARD; PRT; 1655 AA.

OWPE_STANDARD; ONX45;
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Perl. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           569 ------KNTGNATYRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 126; Conservative 64; Mismatches 194; Indels 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.3%; Score 189.5; DB 1; Length 1953; Similarity 23.1%; Pred. No. 0.051;
7.

9.

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11.

12.

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14.

15. (INCOMPLETE).

D -> DRGDDDVTPPDD (IN REF. 1).

A -> R (IN REF. 3).

D -> N (IN REF. 3).

CVLE -> ITLO, (IN REF. 1).

SA -> T (IN REF. 1).

SA -> T (IN REF. 1).
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            166
177
188
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                                                                                                                                                      REPEAT
REPEAT
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CONFLICT
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SEQUENCE
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OMPB_RICCN
ID OMPB_R
AC OGKRA3
DT 16-OCT
DT 01-MAR
DE OUTER 1
DE COUTER 1
DE COU
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-1- CAUTION: Ref. 3 sequence differs from that shown due to frameshifts
in positions 414 and 732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-LTZ / ASCC100720;
STRAIN-LTZ / SGSC112 / ATCC 700720;
MCDLINE-21534948; PubMed-11677609;
MCCLelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu J.Y., Slegel L.M., Kredich N.M.;
"High-level expression of Escherichia coli NADPH-sulfite reductase:
requirement for a cloned cysG plasmid to overcome limiting siroheme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Complete proteome.
POTENTIAL.
POTENTIAL.
PROTEIN SURFACE-EXPOSED VIRULENCE
PROTEIN BIGA.
15 X 11 AA TANDEM REPEATS.
1 (INCOMPLETE).
2 (INCOMPLETE).
3 (INCOMPLETE).
4.
6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                           BIGA_SALTY
PS592R; O9XCG3;
PS592R; O9XCG3;
O1-MAY-1992 (Rel. 22, Created)
O1-MAY-2002 (Rel. 41, Last sequence update)
O1-MAR-2002 (Rel. 41, Last annotation update)
Putartive surface-exposed virulence protein bigA precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stojiljković I., Valentine P., Heffron F.;
"Salmonella typhimurium rhs homolog."
Submitted (MAR-1999) to the EMBL/GenBank/PDBJ databases.
        EMBL, AF133696; AAD39458.1; --
EMBL, AR0808959; AAD2340.1; --
EMBL; M64606; AAA27042.1; ALT_FRAME.
EMBL; M64606; AAA27043.1; ALT_FRAME.
PIR, C392000; C393200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91100301; PubMed-1987123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-765 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:852-856(2001).
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Virulence; Repeat; Sign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
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J. Bacter
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                                                                                                                                                      RESULT 9
BIGA_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Stenos J., Walker D.;

"The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases

--- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR

STRUCTUBAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLUIAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P -> A (IN STRAIN INDIAN TICK TYPHUS).

G -> S (IN STRAIN INDIAN TICK TYPHUS).

K -> N (IN STRAIN INDIAN TICK TYPHUS).

N -> D (IN STRAIN INDIAN TICK TYPHUS).

N -> D (IN STRAIN INDIAN TICK TYPHUS).

N -> D (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

C -> G (IN REF. 3).

E -> D (IN REF. 3).

E -> S (IN REF. 3).

E -> S (IN REF. 3).

H -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                                                                                                                                            "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                    'Phylogenetic analysis of members of the genus Rickettsia using the
                                                                                                                                                             Fournier P.-E., Barbe
                                                                                                                                      MEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
120 KDA SURFACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
OMPB OR RC1085.
Rickettsia conorii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E49E19377D5FCE37 CRC64;
                                                                                                                                                                                                                                                                                                                                                  gene coding the outer-membrane protein rompB (ompB)."; int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                             STRAIN-Indian tick typhus, and Malish 7;
MEDLINE-20393643; PubMed-10939649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF123726; AAF34129.1; --
EMBL; AF140110; AAD39533.1; --
InterPro; IPR003858; COmpA_COmpB.
Pfam; PF02708; rOmpA_rOmpB. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE008659; AAL03623.1; -. EMBL; AF123721; AAF34124.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 353-1655 FROM N.A.
                                                                                                                                                                                                                                                               SEQUENCE OF 33-1649 FROM N.A.
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CHAIN 1 1334
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                                                                                                                                                                                                                                                                                                                   Roux V., Raoult D.;
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                                                                                                       SEQUENCE FROM N.A.
                                                                                                                         STRAIN-Malish 7;
                                                                      NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Malish 7
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Length 1655;

DB 1;

6.2%; Score 186.5;

Query Match

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36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510 LAAGTITLDGSATITGDIGNAGGAAALQGITLANDATKTLTLGGANIIGANGGTINFQAN 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNNIEITRNGKNI----DIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----VAQVNNGAAIDNNDLQGVGRIDCGAAAS--TLVFNLANP-TTQKAPLILGDNAVI 206
                                                                                                                                                                                                                                                                                                173 GDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGT 232
                                                                                                                                                                                                                                                                                                                                                                               233 TASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                             327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 AAGFVVSVDNGKVATIDGQVYAKDMVIQSANAVGQVNFRHIVDVGTDGTTAFKTAASKVA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TANGQTGQADKF------ETVTSGTNVT-FASGKGTTA-TVSKDDQGNI-TVMYD 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TNVAQLKGVAQNLNNRIDNVDG 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NARAGIAQAIATAGLVQAYLPGK-----SMMAIGGGTYRGEAGYA-----IGYSS 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            687 TLATGINLGSAINPLAEINFGSKGAANVDIVLNVG----KGVNLYAINITIDANVGSFI 742
                                                                                              95 NTANNLDVTVREDTTLGFITNVVNNANHFNLMLNAGKTLTITGQGITNVQAAATKNANNV 154
                                                                                                                                        DLYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKI 118
                                                                                                                                                                                                                      119 KONGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTN----- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 -VNGANGTLNVTNGFIKVSS-----KSF-ATVNVINI-GDGQGIMFNTDADNVNTLNLQA
                                                                                                                                                                                                                                                                                                                                     259 NGATITFNGTDGTGRLVLLSKNAA--ATDFNVTG------SLGGNLKGI---
                                                                                                                                                                                                                                                                                                                                                                                                                  ------GANAAVIGTNNG------GANAAVIGTNNG---AGR
                                                           ----RNHTKRASATVKTAVLATLLFATVQASANNEEQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKG-----ENGS-STDEGE------GLVTAKEVIDAVNKAGWRMKTT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374 VNVGDALNVNOLONSGWNLDSKA-----VAGS----SGKVISGNVSPSK----
                77; Mismatches 266; Indels 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia typhi.
Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=785;
Pred. No. 0.058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1645 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            743 FNAGGTNIVSGTVGGQQGNKFNTVA 767
  21.6%;
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                    161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
  Best Local Similarity
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                      Matches
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us-09-700-293-4.rsp

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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION OF CLEAVAGE SITE.

MEDLINE-29104668, pubmed=1729180;

Hacksteadt T., Messer R., Cleplak W., Peacock M.G.;

Hacksteadt T., Messer R., Cleplak W., Peacock M.G.;

Hacksteadt T., Messer R., Cleplak W., Peacock M.G.;

membrane protein of rickettsiae: identification of an avirulent mutant deficient in processing.';

Infect. Inmun. 60:1159-165(1992).

Infect. Inmun. 60:1159-165(1992).

STRUCTURAL THE 120 MED SURPACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIAL VIRULENCE FACTOR AND/OR INMUNOGEN DURING INPECTION.

I- FUNCTION: THE 32 AND BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR. S-LAYER WITH HEXACONAL SYMMETRY.

S-LAYER WITH HEXACONAL SYMMETRY.

I- SIMILARITY: BELONGS TO THE RICKETISIAE OMPA,OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 LAVTINENTILGFVTNVTKQGNFFNFTIGAGKSLTITGHGITAQQAATTKSAQNVVSKVN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 SDWAVYFNE-KGV-------LTAREITLKAGDNLKIKQNGTNFTYSLKK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 AGAAINDNDLSGVGSIDFTAAPSVLEFNLINPTTQEAPLTLGDNAKI-VNGANGILNITN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 ---DLTDLTSVGTEKLSFSAN-GNKVNITSD-TKGLNFAKETAGTNGDTTVHLNGIGSTL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 NHTKRASATV-----KTAVLATLLFAT---VQASANN-----EEQEEDLYLDPV-- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 NRTINAAAITVDGAGFDQIGAGVNLPVAINSVITANSNNAITFNIPNGNLNSLFLDIANT 99
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                                                  MEDLINE-94040787; PubMed-8224886; Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.; "Cloning and sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi."; Gene 133:129-133(1993).
                                                                                                                                                                                                                         STRAIN-WILMINGTON;
MEDILIPS-2114896; PubMed-1370573;
Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sites on CNBr fragments of the S-layer protein antigens of Rickettsia typhi and Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 KDA SURRACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
MEMBRANE ANCHOR (POTENTIAL).
H -> N (IN REF. 2).
V -> I (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
G -> S (IN REF. 2).
G -> S (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.2%; Score 185; DB 1; Length 1645; 21.5%; Pred. No. 0.068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003858; rOmpA_rompB.
708; rOmpA_rompB; 1.
5-layer; Transmembrane; Cell wall.
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657 657
842 842
1071 1071
1306 1306
1645 AA; 169698 M
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                             STRAIN-WILMINGTON;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen; S-layer;
                                                                                                                                                                                                        PARTIAL SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                              prowazekii
Mol. Immun
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CONFLICT
SEQUENCE
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MEDITINE-20150255; PubMed-10684935;
Read T.D., Brunham R.D., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Otterback T., Berry K., Bass S.,
Linher K., Weddman J., Khouri H., Craven B., Bowman C., Dodson R.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 LANDASKILTLSGANIGANAGGAIHFQANGGTIQLTSTQNNILVDFDLDVTTDQTGVVD 600
                                                                            271 TGKLVLVSKNGNATEFNVTG------SLGGNLKGVIEFDTTAAAGKLIANGGA 317
                                                                                                                                                                 235 -----SDN-----VDFVRTYDTVEFLSADTKTTTVNVESKD------NGKKT----- 270
                                                                                                                                                                                                                                    318 ANAVIGTDNGAGRAAGFIVSVD----NGNAATISGOVYAKDIVIQSANAGGOVTFEHLV 372
                                                                                                                                                                                                                                                                                                                          271 EVKIGAKTSVIKEKDGKLVTGKDKGENGS--STDEG------EGLVTAKEVIDAVN 318
                                                                                                                                                                                                                                                                                                                                                                                                      373 DVGLGGKTN-FKTADSKVII----TENASFGSTDFGNLAVQIVVPNNKILLTGNFIGDAKN 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 K---AGWRMKTTTANGQ--TGQADKFETVTS-----GTNVTFASG-----KGTTAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452 LGAGADAPTLSVDGD------ALNVGSKK-------DNKPVRIT- 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 NIYLLITKTINAANQGKIIVAADPINTDTALADGTNLGSAESPLSNIHFATKAANGDSILH 720
187 TDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGV-KPGTTA----- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 -----TPQFSSVS 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 NVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 28:1397-1406(2000).
-1- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0572/CT456/TC0741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae {\rm AR39.}^{\,\rm u}\,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 IGGTYRGEAGYA-----IGYSSISDGGNWIIKGTASG 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBL_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (2-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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us-09-700-293-4.rsp

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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFVVLNG------BEVINKG------FTL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQRTVAVLIVNSDKEGTGEKEKVE--ENSDWAVYFNEKGVLTAREITLKAGDNLKI---K 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDS------GISVALEDNTVRGIVQNEGSIKAGEITLSAKGRKEALDSLVMNNGV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQN-SGWNLD 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223; Indels 124;
                                                             Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                          STRAIN=NTHI N182;
MEDLINE=95115556; PubMed=7815944;
Cope L.D., Thomas S.E., Latimer J.L., Slaughter C.A.,
Mueller-Eberhard U., Hansen E.J.;
"The 100 kDa haem:haemopexin-binding protein of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEME/HEMOPEXIN-BINDING PROTEIN. 3 X 5 AA TANDEM REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7FF39BB8C046539D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.1%; Score 182; DB 1;
illarity 21.3%; Pred. No. 0.048;
Conservative 92; Mismatches 223;
                                                                                                                                                                                                                                                         influenzae: structure and localization.";
Mol. Microbiol. 13:863-873(1994).
-!- FUNCTION: BINDS HEME/HEMOPEXIN COMPLEXES.
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Transport; Signal; Repeat.
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100148 N
                                         Haemophilus influenzae
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Best Local Similarity
Matches 119; Conserv
                                                                                                                                          SEQUENCE FROM N.A.
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224
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                                                                                                NCBI_TaxID=727;
                                                                              Haemophilus.
    protein A).
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    SOURCE STATE STATE STATE SOURCE STATE STATE SOURCE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272
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                                                                                                                                                                                                 Gaps
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16-OCT-2001 (Rel. 40, Last annotation update)
Heme/hemopexin-binding protein precursor (Heme:hemopexin utilization
                                                                                                                                                                                                                                                                                                                                                                                             ------KIKQNGTNFTYSL--KKDLTDLTSV--GTEKLSFSANGNKVN----ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | ::: | | : | | | SLSDVDSRVEDPDGVSDTESTNGNDSGKTTSTEENGDPSGPDILAAVRKHLDTVYPGENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SGNVSPSKGKMDETVNINAGNNI-EITRNGKNIDIATSMTP----QFSSVSLGAG
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                                                                                                                                                                                                 248;
                                                                                                                                                            Length 1007;
                                                                                                                                                                                                                                                                                                                   -KEGTGEKEKVEE-------NSDWAVYFNEKGVLTAREITLKAGDNL-
                                                                                                                                                        6.1%; Score 183; DB 1; Length 10
Larity 21.5%; Pred. No. 0.048;
Conservative 85; Mismatches 238; Indels
                                                                            HYPOTHETICAL PROTEIN TC0741 IN; 842800C0871B1518 CRC64;
                                                                                                                                                                                                                                      SATVKTAVLATLLFATVQASANNEEQEEDLYLDPVQRTVAVLIVNSD----
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                                       Complete proteome.
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                                                                                              1007 AA; 104006 MW;
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                                     Signal;
EMBL; AE002342; AAF39550.1;
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                                     Hypothetical protein; SIGNAL 1 51
                                                                          1007
                                                                                                                                                                             Similarity
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P45355;
01-NOV-1995
                                                                                                                                                        Query Match
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Matches 156;
                                                                                              SEQUENCE
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ID HXA3_H;

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DT 01-NOV

DT 01-NOV

DT 16-OCT

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                    394 S------KAVAGSSGKV-----ISGNVS------PSKGKMD-ETVNINA 424
                                                                                                                                                                                                    | :: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVAPGVKEGDVTNVAQLKGVAQNLNNRIDNV---DGNARAGIAQAIATAGLVQAYLPGKS 539
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325 TSPKINFKGKSVNINGNFGRENSGTHYNEERKTLNTEVNIDVPGAENIRIADDKDNTETD 384
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16-0CT-2001 (Rel. 40, Last annotation update)

30.0ter membrane protein B precursor (168 kDa surface-layer protein)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uchiyama T.; "Sequencing of the gene encoding the protein rOmp B of Rickettsia 'abonica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%; Score 181; DB 1; Length 1656;
21.9%; Pred. No. 0.11;
vative 80; Mismatches 284; Indels 202;
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-I-FUNCTION: THE 120 KDA SURRAGE-ENFOSED PROTEIN 13 A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
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32 KDA BETA PEPTIDE.
POLY-GLY.
WW: 3132A69C9DD5999F CRC64;
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InterPro; IPR003858; rompA_rompB.
Pfam; PF02708; rompA_rompB; 1.
Antigen; S-layer; Cell wall.
CHAIN
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35;

Gaps

Conservative

Best Local Similarity Matches 159; Conserv

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-----AQNIVAKFNGGAAIANNDLSGLG---TIDFGAAASTLVFDLANPTTQKAPLILA 201
                                                                                                                                                  114 DNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTN- 172
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01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Heme/hemopexin-binding protein precursor (Heme:hemopexin utilization
10 NSALNAWVAVSELT-----RNHTKRASATV---KTAVLATLLFATVQASANNEEQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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TRAIN-DIA2. 7 SEROTYPE B;
MEDLINE-95115556; PUDMed-7815944;
COPE L.D., Thomas S.E., Latimer J.L., Slaughter C.A.,
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P45354:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|::| |: :: || | : :: || 63 FDIGQKKEVKFEQPNEHAVAYNRVIGGNASQIQGKLTANGKVYLANPNGVITQGAEINV
                                                                                                                                Cope L.D., Yogev R., Mueller-Eberhard U., Hansen E.J.;
"A gene cluster involved in the utilization of both free heme and heme:hemopexin by Haemophilus influenzae type b.";
J. Bacteriol. 177:2644-2653(1995).
-!- FUNCTION: BINDS HEME/HEMOPEXIN COMPLEXES.
-!- SUBCELLULAR LOCATION: Secreted.
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6 X 6 AA APPROXIMATE REPEATS.
1-1.
1-2.
1-3.
1-4.
1-5.
1-6.
4 X 6 AA APPROXIMATE TANDEM REPEA
2-1.
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Mueller-Eberhard U., Hansen E.J.; The 100 Kba haem:haemopexin-binding protein of Haemophilus influenzae: structure and localization."; Mol. Microbiol. 13:863-873(1994).
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                                                                                                  STRAIN-DL42 / SEROTYPE B;
MEDLINE-95270579; PubMed-7751272;
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Matches 127; Conserv
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STRAIN-DL42
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                                                   ••••-NIDIATSMTPQFSSVSLGAGADAPTLSVDGDALN-----VGSKKDNKPVRITN
408 NVS---PSKGKMD---ETVNI-
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Search completed: September 5, 2002, 10:31:09 Job time: 436 sec

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1 MNKIYRIIWNSALNAWVAVS.....TASGNSRGHFGASASVGYQW
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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09JPS6
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sp_unclassified:*
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## ALIGNMENTS

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ш	PROTEIN).									
z	GNA992 OR NMB0992 OR NHHA.	HA.								
s	Neisseria meningitidis,	and								
S	Neisseria meningitidis (serogroup B).	(serog	roup B).							
U	Bacteria; Proteobacteria; beta subdivision; Neisserlaceae; Neisseria.	a; bet	a subdiv	isic	n; Nei	sseria	ceae;	Neiss	eria.	
×	NCBI_TaxID=487, 491;									
z	[1]									
Д	SEQUENCE FROM N.A.									
ບ	STRAIN=MC58 / SEROGROUP	B, B2	169, BZB	3, 7	BZ83, AND H44/76;	/16;				
×	MEDLINE-20175756; PubMed-10710308;	d=1071	0308;							
A	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,	Masign	ani V.,	Giu]	Liani M	.M., A	rico,	В.,		
Æ	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,	G.T.,	Baldi I	:	3artoli	ni E.,	Capec	chi B		
A	Galeotti C.L., Luzzi E.	, Mane	tti R.,	Marc	shetti	E., MO	ra M.,	, Nuti	S	
Æ	Ratti G., Santini L., S	avino	S., Scar	se]]	li M.,	Storni	Ε., 2	Suo P.		
Æ	Broeker M., Hundt E., K	napp B	., Blair	ш	Mason	T., T	etteli	In H.,		
A	Hood D.W., Jeffries A.C	., Sau	nders N.	٦.,	Granof	f D.M.	, Vent	er c.	,	
Ą	Moxon E.R., Grandi G., Rappuoli R.;	Rappuo	li R.;							
H	"Identification of Vaccine Candidates Against Serogroup B	ine Ca	ndidates	Age	ainst S	erogro	g dn			
E+	Meningococcus by Whole-Genome Sequencing.";	Genome	Sednenc	ing	·`					
ᆸ	Science 287:1816-1820(2	000)								
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ပ	STRAIN-MC58 / SEROGROUP	В;								
×	MEDLINE-20175755; PubMed-10710307;	d=1071	0307;							
A	Tettelin H., Saunders N	J., H	eidelber	9 J.	, Jeff	ries A	,	Velson	K.E	
Ą	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,	., Hoo	d D.W.,	Pede	en J.F.	, Dods	on R.J	· .		
Ą	Nelson W.C., Gwinn M.L.	, DeBo	у К., Ре	ters	son J.D	., Hic	key E.	χ.,		
¥	Haft D.H., Salzberg S.L	., Whi	te 0., F	lei	schmann	R.D.,	Doug	nerty	B.A.	-
Ą	Mason T., Ciecko A., Pa	rksey	D.S., Bl	air	E., Ci	ttone	H., C.	lark E	.В.,	
A	Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,	T.R.,	Khouri H	<u>`</u>	)in H.,	Vamat	hevan	٦.,		
A	Gill J., Scarlato V., M	asigna	ni V., F	izzā	м., G	randi	G., St	ın L.,		

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Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) OUTER MEMBRANE PROTEIN GNA992.
                                                                                                STRAIN=B2147;
MEDLINE=20175756; PubMed=10710308;
                                                                                     SEQUENCE FROM N.A.
                                                              NCBI_TaxID=487;
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unith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                  SPECIES-N menigitidis; STRAIN-PMC21;
SPECIES-N menigitidis; STRAIN-PMC21;
BAGA I.R., Stikhanta Y., Disckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer membrane protein of Neissoria meningitidis";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR226375; AAR41395.1;
EMBL; AR226370; AAR42519.1;
EMBL; AR226370; AAR42519.1;
EMBL; AR226370; AAR42519.1;
EMBL; AR226370; AAR42519.1;
EMBL; AR226371; AR425211;
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Pred. No. 1.9e-118;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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99.88;
                                   science 287:1809-1815(2000).
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Best Local Similarity 99.8
Matches 590; Conservative
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Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Capcanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galectti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Batti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Brocker M., Hundt E., Khapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., "Identification of Vaccine Candidates Against Serogroup B Meningococus by Whole-Genome Sequencing.";

EMBL: AF226366; AR42215.1; -. SEQUENCE S91 AA; 62113 MW; 533453CAE5A91EIF CRC64;
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subdivision; Neisserlaceae; Neisserla
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Pred. No. 4e-117;
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Bacteria; Proteobacteria;
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                                                                                                                        Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P. "Identification and characterization of a gene encoding a novel membrane protein of Nelsseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFIS/6006, AAK68067.1;
SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;
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SC-2001 (TrEMBLrel. 19; Created)
SC-2001 (TrEMBLrel. 19, Last sequence update)
SC-2001 (TrEMBLrel. 19, Last annotation update)
OUTER MEMBRANE PROTEIN.
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Pred. No. 1.2e-117;
1; Mismatches 3;
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Best Local Similarity 99.3%;
Matches 587; Conservative 1
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                                                        Neisseria meningitidis
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                                                                             NCBI_TaxID=487;
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01-DEC-2001 (
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STRAIN-MC58;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P. Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P. Tidentification and characterisation of a gene encoding a novel membrane protein of Neissaria meningitidis."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR125375; AAK09243.1; -. EMBL; AR125375; AAK09243.1; -.
                                                                                                                                                                                 Length 592;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLR PROTEIN.
NHAA OUTER MEMBRANE PROTEIN.
NHAA
NEISseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID-487;
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                    Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comadducia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Gomadducia M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Hood D.W., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Moxon E.R., Grandi G., Rappuoli R.; Tendif D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.; Tendification of Vaccine Candidates Against Serogroup B. Meningococcus by Whole-Genome Sequencing:";
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SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;
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         MEDLINE=20175756; PubMed=10710308;
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STRAIN-NGE28;
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Peak I.R., Sikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Pldentification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to TEBL/GenBank/DDBJ databases.
EMBL: ARIS7605; AAK68866.1; -.
SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3ABEA2 CRC64;
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MEDLINE-20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico'
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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EMBL: AF226371: AAR42520.1; -
SEQUENCE 600 AA; 62762 MW; 36256963E059BCDI CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                             91.8%; Score 2757.5; DB 2;
91.5%; Pred. No. 2.5e-108;
iive 14; Mismatches 26;
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Best Local Similarity 91.55
Matches 550; Conservative
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                                                                 Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galecti C.L., Luzzi E., Maneti R., Marchetti E., Mora M., Nuti S., Bratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.; Alderification of Vaccine Candidates Against Serogroup B. Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).

EMBL, AF226376; AAF42525.1; BEMBL, AF226389, AAF425181.; SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 2751.5; DB 2; Pred. No. 4.4e-108; 13; Mismatches 23;
SEQUENCE FROM N.A.
STRAIN-NG3/88, AND BZ232;
MEDLINE-20175756; Pubmed=10710308;
                                                                                                                                                                                                                                                                                                                                                                                                            91.6%;
92.1%;
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Best Local Similarity 92.1%
Matches 551; Conservative
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GNA992 OR NHHA.
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                                                      PEQUENCE FROM N.A.

STAIN=NCB231;

STAIN=NCB231;

NEDLINE-20175756; PubbWed-10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Commducci M., Jennings G.T., Baldi L., Bartolini E., Capecohi B.,

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Rabcote M., Hundt E., Knapp B., Blair E., Mason T., Tettellin H.,

Rock M., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Raboro E., Grandi G., Rappuoli R.,

Mond D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Rabingococcus by Whole-Genome Sequencing.",

Science 287:1816-1820(2000).

Seguence 287:1816-1820(2000).

SEQUENCE 594 AA; 62114 WW; 1E2A63A78FS3D256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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Matches 550; Conserv
                                NCBI_TaxID=487;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=487;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN)
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                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=BZ198, AND 297-0;
MEDLINE=20175756; PubMed=10710308;
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SEQUENCE FROM N.A.
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STRAIN=2996;
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NCBL_TaxID=487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL, AF226382; AAF42531.1; .
SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;
                                                                                                                                                              (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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MEDLINE-20175756; Pubmed-10710308;
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                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                           Neisseria meningitidis
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SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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; Pred. No. 8e-107;
13; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN (BNA992.
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Science 287:1816-1820(2000).
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Best Local Similarity 90.7'
Matches 546; Conservative
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SEQUENCE FROM N.A.
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STRAIN=H15;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226381; AF425301; -
EMBL; AF256381; AF425301; -
EMBL; AF256381; -
EMBL; AF256381; -
SEQUENCE 598 AA; 62763 MW; E6C7AEF0BBBA63CB CRC64;
                              470 VGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG 529
                                                                                                                                530 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY 589
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PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALN 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis.
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID-487;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
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MEDLINE=20175756; PubMed=10710308;
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177 TNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 236
                                                    231 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVT 290
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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ASGNGTTATVSKDDQGN1TVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKV1SGNVS
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                                             GKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF
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0UTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennin "Identification and characterization of a gene encoding membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF226383, AF8425321;
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SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;
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US-09-700-293-4 3003 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASASVGYQW 591 Title: Perfect score: Sequence:

Scoring table: F.BLOSUM62 Gapop 10.0 , Gapext 0.5 Gapop 10.0 , Gapext 0.5 Searched: 231628 segs, 24425594 residues

Total number of hits satisfying chosen parameters:

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### SUMMARIES

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944	Sequence 32, Appl Sequence 2, Appli	32,	Sequence 32, Appl Sequence 44, Appl	ທັທ	5,7	Sequence 15, Appl Sequence 26, Appl	Sequence 30, Appl	Sequence 24, Appl	Sequence 28, Appl
US-08-913-942-6 US-08-409-995-4 US-08-685-467-4	US-09-268-347-32 US-08-409-995-2	US-08-083-407-2 US-09-377-155-32 US-08-913-942-2	US-09-669-974-32 US-09-268-347-44	US-08-409-995-5	US-08-913-942-5	US-08-913-942-15 US-09-268-347-26	US-09-268-347-30	US-09-268-347-24	US-09-268-347-28
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607 1912 1912	1094	1098	1098	658	658	679	1004	1002	1104
39.3 39.3	35.6	35.2	35.2	34.6	34.6	33.1	25.1	24.7	23.2
1180.5 1180.5 1180.5	1070.5	1057.5	1057.5	1039.5	1039.5	995	752.5	741.5	696.5
28 29 30	31	34	36	300	40	41	43	44	45

## ALIGNMENTS

RESULT 1 US-09-377-155-21

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ORGANISM: Neisseria meningitidis US-09-669-974-21

; 0 Gaps : **;** Query Match
99.9%; Score 2999; DB 4; Length 591;
Best Local Similarity 99.8%; Pred. No. 6.7e-225;
Matches 590; Conservative 0; Mismatches 1; Indels

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181 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF  241 VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS 300 [24] VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGARTSVIKEKDGKLVTGKDKGENGSS 300 TDEGEGLUTAKEVIDAVNKAGWRMKTTTANGGTGQADKFETVTSGTNVTFASGKGTTATV 360

301 IDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 360 361 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV 420 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR 480 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM 540 BEST AVALAGE COPY 481 δλ g Qγ qq δλ a Qγ q

APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
ITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: CT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14 Sequence 11, Application US/09377155 Patent No. 6197312 TYPE: PRT ORGANISM: Neisseria meningitidis PatentIn Ver. 2.0 33 NUMBER OF SEQ ID NOS: SOFTWARE: PatentIn Ve GENERAL INFORMATION: US-09-377-155-11 US-09-377-155-11 LENGTH: 591 SEQ ID NO 11

61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120 NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF 240 241 VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS 300 301 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 360 1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60 ö Score 2980; DB 4; Length 591; Pred. No. 2e-223; 3; Indels 1; Mismatches 99.2%; Best Local Similarity 99.3 Matches 587; Conservative 121 301 ò g ò g ò g q δ 엄 ò g ò

361 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV 420

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Query Match

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